

GenCore version 5.1.6
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M nucleic - protein search, using frame_plus_n2p model

un on: March 9, 2004, 08:52:43 ; Search time 153 Seconds

(without alignments)
12805.127 Million cell updates/sec

itle: US-09-719-272-1

erfect score: 1138

equenece: 1 gatccggactgaagactccc.....atttgataatcagatttct 3467

coring table:

OLIGO 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

searched: 1586107 seqs, 282547505 residues

ord size: 1

total number of hits satisfying chosen parameters: 2987630

minimum DB seq length: 0

maximum DB seq length: 2000000000

ost-processing: Listing first 45 summaries

ommand line parameters:

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Q/cgn2_1/USPTO.spool_p/US09719272/runat_09032004_085229_7428/app_query.fasta_1.3655
DB=A Geneseq 29Jan04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
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NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -USFBLCK=100 -LONGLOG
DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

database :

A Geneseq 29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	607	53.3	607	3	RAY81783 Human pro
2	607	53.3	607	3	RAY56098 LAR tyros
3	607	53.3	647	4	RAM23746 Human EST
4	607	53.3	647	4	AAU14379 Human nov
5	607	53.3	1796	6	AAE37971 Human kin
6	607	53.3	1897	3	RAY81785 Human pro
7	607	53.3	1897	3	RAY56100 LAR tyros
8	607	53.3	1897	3	AAU19712 Human pro
9	607	53.3	1897	7	ADD18740 Human dis
10	607	53.3	1907	4	AAU14143 Human nov

11	442	38.8	442	3	AA556372	AA556372 Human pro
12	296	26.0	296	7	ABW78984	ABW78984 Human leu
13	202	17.8	306	4	AA678268	AA678268 Human DCA
14	197	17.3	294	4	AA678287	AA678287 Human BCA
15	141	12.4	250	4	AA593370	AA593370 Human pro
16	136	12.0	245	4	AA593389	AA593389 Human pro
17	59	5.2	1501	2	AA672858	AA672858 Rat recep
18	59	5.2	1863	7	ADD46989	ADD46989 Rat Prote
19	59	5.2	1904	5	ABBS7100	ABBS7100 Mouse isc
20	59	5.2	1911	2	AA671726	AA671726 Human ptp
21	59	5.2	1911	2	AAW27225	AAW27225 Human pro
22	59	5.2	1911	2	AAW94027	AAW94027 Human pro
23	59	5.2	1911	4	AAU01459	AAU01459 Human pro
24	59	5.2	1948	7	ADD18742	ADD18742 Human dis
25	59	5.2	1949	7	ADE57117	ADE57117 Human pro
26	59	5.2	1949	7	ADE57121	ADE57121 Human pro
27	59	5.2	1949	7	ADD47019	ADD47019 Human pro
28	59	5.2	1949	7	ADD47015	ADD47015 Human pro
29	54	4.7	1291	2	AA675201	AA675201 Tyrosine
30	44	3.9	154	2	AA56458	AA56458 Murine pr
31	40	3.5	1496	5	ABBS7380	ABBS7380 Rat mucoc
32	40	3.5	1496	7	ADE57115	ADE57115 Rat Prote
33	40	3.5	1496	7	ADE57119	ADE57119 Rat Prote
34	40	3.5	1496	7	ADD47013	ADD47013 Rat Prote
35	40	3.5	1496	7	ADD47017	ADD47017 Rat Prote
36	34	3.0	2037	4	ABBS71928	ABBS71928 Drosophil
37	14	1.2	14	2	AA67006	AA67006 LAR prote
38	14	1.2	176	2	AA60876	AA60876 Product o
39	14	1.2	322	2	AA60877	AA60877 Mouse ptp
40	14	1.2	405	2	AAW89251	AAW89251 Mouse PTP
41	14	1.2	426	2	AAW89249	AAW89249 Mouse PTP
42	14	1.2	463	2	AAW89250	AAW89250 Mouse PTP
43	14	1.2	1959	6	AAE37322	AAE37322 Human rec
44	14	1.2	2281	5	AAO18736	AAO18736 Human NOV
45	14	1.2	2291	6	ABP60057	ABP60057 Human pho

ALIGNMENTS

RESULT 1

AA556372
ID AA556372 standard; protein; 607 AA.

XX AA556372;

AC AA556372;

DT 07-JUN-2000 (first entry)

XX Human protein tyrosine phosphatase specific antibody protein sequence.
DE Human; protein tyrosine phosphatase; antibody; intracellular domain; LAR;
KW CD45; PTP; diagnosis; insulin resistance related disease; syndrome X;
KW non-insulin dependent diabetes mellitus; arteriosclerosis; therapy;
KW heart disorder.

OS Homo sapiens.

XX WO200002922-A1.

XX 20-JAN-2000.

XX 06-JUL-1999; 99WO-JP003856.

XX 10-JUL-1998; 98WO-JP003120.

XX (FUSO) FUSO PHARM IND LTD.

XX Yamamoto H, Tsujikawa K, Uchino Y;

XX WPI; 2000-182215/16.

XX N-PSDB; AA291907.

PT Antibody for diagnosis and treatment of insulin resistance disorders and

PT syndrome X recognises the intracellular domains of tyrosine kinases.

241	Ala	Gly	Pro	Met	Val	His	Cys	Ser	Ala	Gly	Val	Gly	Arg	Thr	Gly	Cys	Phe	Leu	Val	260	
786	ATT	CAT	CGC	CAT	GTG	CAG	CGG	ATG	GAAC	CAC	GAG	AAG	CGG	TGG	ACA	TCT	ATG	GCC	CAC	GTC	845
261	Ile	Asp	Ala	Met	Leu	Glu	Arg	Met	Val	His	Glu	Val	Thr	Val	Asp	Ile	Tyr	Gly	His	Val	280
846	ACT	GCA	TGC	GAT	CA	CAG	AGA	CTA	CTA	TGT	GTC	CAG	CGG	AGG	CAC	GAG	CGT	GTT	CAT	C	905
281	Thr	Cys	Met	Arg	Ser	Gln	Arg	Asn	Tyr	Met	Val	Gln	Thr	Glu	Asp	Gln	Tyr	Val	Phe	Leu	300
906	CAT	GAG	CGC	TGT	GAG	GCT	CC	CAT	CGT	CGG	CCA	CAC	GAG	GTC	GCT	GGC	CCG	CAA	CCT	G	965

966	TATGCCACATCCAGAAAGCTGGCCAAAGTGCTCCAGGGGAGAGTGTACCGCCATGGAG	1025
QY		
321	TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMetGlu	340
Db		
1026	CTCAGATTCAAGTTGTGGCCGAGCTCCAAAGGCCACACAGTCTCCGCTTCATCAGGGCCAAC	1085
QY		
341	LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn	360
Db		

361	LeuProCysAsnLysPheLysAsnArgLeuValAsnLleMetProTyrGluLeuThrArg	380
1146	GTGTGCTGCAGCCCATCCGTTGGTGTGGAGGCTCTGACTACATCAATGCCAGCTTCCTG	1205
381	ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu	400
1206	GATGGTTATAGACAGCAGAGGCCTACATAGCTACACAGGGGCTCTGGCAGACAGACCC	1265
401	AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr	420
1266	GAGGACTTCTGGCGCATGCTATGGGAGCACAAATCCACATCATGCTCATGCTGACCAAG	1325
421	GluAspPheIrpArgMetLeuTrpGluHisAsnSerThrIleIleValMetLeuThrLys	440
1326	CTTCGGAGATGGCAGGAGAAATGCCACAGTACTGCCAGACAGAGCGCTCTGCTCGC	1385
441	LeuArgGlnMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg	460
1386	TACCAGTACTTGTGTGACCCGATGGCTGAGTACAAATGCCGCCAGTATATCCTCGGT	1445
461	TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg	480
1446	GAGTCTCAGGTCACGATCCCGGATGGCACTCAAGGCAATCCGCACTCCAGTTC	1505
481	GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe	500
1506	ACAGACTGGCCAGACAGCGCGCTGCCCAAGACAGCGAGGATTCATGACTTCATCGGG	1565
501	ThrAspTrpProGlnGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly	520
1566	CAGGTGCATAGACCAAGGACGAGTTGGACAGGATGGCTATCACGTCACGTGCAGT	1625
521	GlnValHisLysThrLysGluGlnPheGlyGlnSerArgProIleThrValHisCysSer	540
1626	GCTGCGCTGGCGCCGACCGCGGTGTTCATCACTCTGAGCATGCTCCTGGAGCGCATCGC	1685
541	AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg	560
1686	TATGAGCGGTGTCGATGTTTCAGCCGCGAGACCCCTCGGTACACAGCGTCTCGCC	1745
561	TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla	580
1746	ATGCTGCAGACAGAGACCAAGTATCAGCTGTGCTACCGTGGCGCCCTGGAGTACTCGGC	1805
581	MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly	600
1806	AGCTTTGACCACTATGCAACG	1826

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b      601 SerPheAspHisTyrAlaThr 607
RESULT 2
AY56098
D      AAY56098 standard; protein; 607 AA.
C      AAY56098;
X      T
X      T 17-APR-2000 (first entry)
E      LAR tyrosine phosphatase intracellular domain.
E      Intracellular domain; P-subunit; human; leucocyte antigen related; LAR;
N      Tyrosine phosphatase; antibody; thyroid cancer.
S      Homo sapiens.
X      X WO9964591-Al.
N      X
D      D 16-DEC-1999.
D      D
F      F 07-JUN-1999; 99WO-JP003054.
R      R 08-JUN-1998; 98WO-JP002542.
X      X
A      A (FUSO ) FUSO PHARM IND LTD.
I      Yamamoto H, Tsujikawa K, Uchino Y, Konishi N;
I      WPI; 2000-097539/08.
R      N-PSDB; AA259132.
T      Antibody recognizing the intracellular domain of the human tyrosine
T      phosphatase LAR.
T      Claim 4; Page 73-78; 104pp; Japanese.
S      X
C      This sequence represents the intracellular domain (P-subunit) of the
C      human leucocyte antigen related (LAR) tyrosine phosphatase (complete
C      sequence in AY56098). The invention relates to the generation of an
C      antibody recognizing the intracellular domain of the human LAR tyrosine
C      phosphatase. The antibody is used for the diagnosis and treatment of
C      thyroid cancer
X      X
Q      Sequence 607 AA;

Ligment Scores:
red. No.: 0 Length: 607
core: 607.00 Matches: 607
Percent Similarity: 100.00% Conservative: 0
Local Similarity: 100.00% Mismatches: 0
Query Match: 53.34% Indels: 0
B: 3 Gaps: 0

S-09-719-272-1 (1-3467) x AAY56098 (1-607)
Y      6 GGACTCAAGGACTCCCTGTGGCCCACTCTCTGACCTGTGGAGATGGAGGCTCAAC 65
b      1 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgLeuLeu 20
Y      66 TACCAGACCCAGGTATGGAGACCAACCCACCCATCCCATCCGACCTGGCGGACAAAC 125
b      21 TyrGlnThrProGlyMetArgAspHisProIleProIleThrAspLeuAlaAspAsn 40
Y      126 ATGAGCGGCTCAAGCCACGATGGCCCTCAAGTCTCCAGAGATGATGATCCATCGAC 185
b      41 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAsp 60
Y      186 CTGGGACAGCAGTTACGTTGGGAGAAATTCAACTCGAGGTGAACAAGCCCAAGAACCGC 245
b      61 ProGlyGlnGlnPheThrTyrGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 80
Y      246 TATGCGAATGTGATCGCCTACGACCACTCTCGAGTCATCTCTTACCTCTATCGATGGCGTC 305

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Db      381 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 100
QY      306 CCGGGAGTGACTATCAATGCACTACATCGATGGCTACCGCAGCAGCAATGCTTAC 365
Db      101 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 120
QY      366 ATCGCCACGACGGGCCCTGCGCGAGACCATGGGCGATTCTTGAGAGATGGTGGGAA 425
Db      121 IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTyrArgMetValTyrGlu 140
QY      426 CAGCGCAGCGCCTGCTGTGATGATGACACGGCTGGAGAGAGTCCCGGTAAATGT 485
Db      141 GlnArgThrAlaThrValValMetMetThrArgLeuGluGluLysSerArgValLysCys 160
QY      486 GATCAGTACTGGCCAGCGCTGGCAGACCATGGGCGATTCTTATTCAGGTGACCTGTG 545
Db      161 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 180
QY      546 GACACAGTGGAGCTGGCCACATACACTGTGCGCACCTTCGCACTCCACAAAGAGTGGCTCC 605
Db      181 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 200
QY      606 AGTGAGAGCGGTGAGCTGGGTCACTGTTTCAGTTTCATGGCTGGCGCACCATCGAGTTCT 665
Db      201 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 220
QY      666 GAGTACCCCACTCCCATCTCTGGCTTCTTACGACGGGTCAAGGCTTCGACCCCTAGAC 725
Db      221 GluTyrProThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp 240
QY      726 GCGAGGCCATGCTGGTGCACCTGACGGCGGGCGGTGGCGGCGGCTTCATCGTG 785
Db      241 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 260
QY      786 ATTGATGCCATGTTGGAGCGGATGAAGCACGAGACGCGTGACATCTATGGCCACGTG 845
Db      261 IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisVal 280
QY      846 ACCTGCTGATGATCAGAGGAACTACATGCTGGTGCAGACGAGGACGACCTGTTCTATC 905
Db      281 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 300
QY      906 CATGAGCGCTGCTGGAGGCTGCCAGCTGCGGCCACACACAGAGGTGCTGCCGCCAACCTG 965
Db      301 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 320
QY      966 TATGCCCATATCCAGAGCTGGCCCAAGTGCCTCCAGGGGAGAGTGTGACCGCATGGAG 1025
Db      321 TyrAlaHisIleGlnLysLeuGlyGlnValProGlyGluSerValThrAlaMetGlu 340
QY      1026 CTGAGTTCAAGTTGCTGGCCAGCTCCAGGCCACACACGTCCTTCATCAGCGCAAC 1085
Db      341 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 360
QY      1086 CTGCGCTGCAACAAAGTTCAAGAACCGGCTGTGTGAACATCATGCGCTACGATGACCCGT 1145
Db      361 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 380
QY      1146 GTGTGTCTGACAGCCATCCGTGTGTGGAGGGCTCTGACTACATCAATGCCAGCTTCCTG 1205
Db      381 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu 400
QY      1206 GATGTTTATAGACGACGAGGCTCATAGTGTACACAGGGGCTCTGGCAGAGACACC 1265
Db      401 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr 420
QY      1266 GAGGACTCTGGCGCATCTGCTGGAGGCAAAATCCACCATCATCTGCTGCTGACCAAG 1325
Db      421 GluAspPheTrpArgMetLeuTyrGluLysAsnSerThrIleIleValMetLeuThrLys 440
QY      1326 CTTGCGGAGATGGCGAGGAGAAATGCAACAGTACTGGCCAGCAGAGCGCTCTGCTCGC 1385

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Db 441 LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 460
1386 TACCAGTACTTTGTTGTTGACCCGATGGCTGAGTACAAATGCCCCAGTATATCTCTGCGT 1445
Db 461 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 480
1446 GAGTTCAGGTACAGTATGCCCGGATGGCAGTCAAGGACATCCGGCAGTCCAGTTC 1505
Db 481 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 500
1506 ACAGACTGGCCAGACAGCGGGCGTCCCAAGACAGCGGCGAGGATTCATTGACTTCATCGGG 1565
Db 501 ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 520
1566 CAGTGCATAGACCAAGAGACAGTTCAGAGATGGGCTATCAGGTGCACTGCAGT 1625
Db 521 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 540
1626 GCTGGCGTGGCCCGACCGGGGTCTTCATCATCTGAGCATCGTCTGGAGCGCATCGCG 1685
Db 541 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 560
1686 TATGAGGGCGTGTGCGACATGTTTCAGACCGTGAAGACCCCTGGGTACACAGCTCTGCG 1745
Db 561 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 580
1746 ATGTTGCGACAGAGGACCATATCATGCTGTGCTACCGTGGCGGCTGGAGTACCTCGCG 1805
Db 581 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly 600
1806 AGCTTTGACCACTATGCAAGC 1826
Db 601 SerPheAspHisTyrAlaThr 607

RESULT 3

AA23746

ID AA23746 standard; protein; 647 AA.

XX AC

XX AA23746;

XX 12-OCT-2001 (first entry)

XX Human EST encoded protein SEQ ID NO: 1271.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

XX diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;

XX gene therapy; nutrition.

XX Homo sapiens.

XX WO200154477-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US002687.

XX 25-JAN-2000; 2000US-00491404.

XX 17-JUL-2000; 2000US-00617746.

XX 03-AUG-2000; 2000US-00631451.

XX 15-SEP-2000; 2000US-00663870.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

XX Cao Y, Drmanac RA, Zhang J, Werhman T;

XX WPI; 2001-476164/51.

XX N-PSDB; AAH98405.

XX Isolated polypeptide for treatment of diseases, diagnostics, raising

XX antibodies and research use.

XX

PS Claim 20; Page 916-917; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention

XX Sequence 647 AA;

SQ

Alignment Scores:

Pred. No.: 0

Score: 607.00

Length: 647

Matches: 607

Percent Similarity: 100.00%

Conservative: 0

Best Local Similarity: 100.00%

Mismatch: 0

Query Match: 53.34%

Indels: 0

Gaps: 0

DB:

US-09-719-272-1 (1-3467) x AA23746 (1-647)

QY 6 GGACTGAAGGACTCTTCTGCTGGCCCACTCTCTGACCTGTGGAGTGGGAGCTCAAC 65

Db 41 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgLeuAsn 60

QY 66 TACCAGACCCAGAGTATCGGAGACACCCACCCATCCCATCCAGCTGGCGGCAAC 125

Db 61 TyrGlnThrProGlyMetArgAspHisProIleThrAspLeuAlaAspAsn 80

QY 126 ATCGAGCGCTCAAGCCCAACGATGGCTCAAGTCTCCAGGAGTATGATCGCTCGAC 185

Db 81 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAsp 100

QY 186 CTGGACAGCAGTTCACGTGGGAGAAATCAAACTGAGGTGAACCAAGCCCAAGACCGC 245

Db 101 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 120

QY 246 TATCGAATGTCATCGCTACGACCATCTCTCGAGTATCTTACTCTATCGATGGGTC 305

Db 121 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 140

QY 306 CCGGGAGTGACTACATCAATGCCAATCATCATCGTGTACCGCAAGCAGATGCTTAC 365

Db 141 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 160

QY 366 ATCGCCACGCGGGCCCTCCCTCCGAGACCATGGCGGATTTCTGAGAAATGCTGGGAA 425

Db 161 IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTyrArgMetValTrpGlu 180

QY 426 CAGCCGACGGCCACTGTGTCATGATGACGGCTGGAGGAGAGTCCCGGTAAAATGT 485

Db 181 GlnArgThrAlaThrValMetMetThrArgLeuGluLysSerArgValLysCys 200

QY 486 GATCAGTACTGGCCAGCCGCTGGCACCAGACCTGTGGCTTATTCAGGTGACCTGTG 545

Db 201 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 220

QY 546 GACACAGTGGAGCTGCCACATACACTGTGGCAGCTTCGCACTCCCAAGAGTGGCTCC 605

Db 221 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 240

QY 606 AGTGAAGCGTGAGTGGCTGAGTTCAGTTTCAGTTCATGGCTGGCCAGACCATGGAGTTCCT 665

Db 241 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTyrProAspHisGlyValPro 260

QY 666 GAGTACCCGAACCTCCATCTGCTGCTTCTTACAGCGGTCAAGGCTCAAGCCCTAGAC 725

Db 261 GluTyrProThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp 280

QY 726 GCAGGCGCCCATGCTGTGCTGCACTGACGCGGGCGTGGCCCGCACCGCTGCTTCATCTG 785

281 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 300
2y
786 ATTGATGCCATGTTGGAGCGGATGAGACGAGACGCGTGGACATCTATGCGCACGTTG 845
2y
301 IleAspAlaMetLeuGluArgMetCysHisGluGlyThrValAspIleTyrGlyHisVal 320
2y
846 ACTGTCATGTCATCAGAGAACTACATGTCGTCAGCGAGGACGACGATGCTGTTTCATC 905
2y
321 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 340
2y
906 CATTGAGCGCTGCTGGAGGCTGCGAGTGGCGCCACACAGAGGTCGTCGCGCAACCTG 965
2y
341 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 360
2y
966 TATGCCACATCCAGAGCTGGGCGAAGTCCCTCCAGGGGAGAGTGTGACCGCATGAG 1025
2y
361 TyrAlaHisIleGlnLysLeuGlyGlnValProGlyGluSerValThrAlaMetGlu 380
2y
1026 CTGAGTTCAGTTCGTCGCGCAGCTCCAGGCGCCACAGCTCCGCTTCATCAGCGCAAC 1085
2y
381 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 400
2y
1086 CTGCGCTGCAACAGTTCAAGAACCGGCTGGTGAACATCATGCCCTACGAATGACCGT 1145
2y
401 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 420
2y
1146 GTGTGCTGTCAGCCATCCGCTGGTGGAGGCTCTGACTACATCATGCTCCAGCTTCCTG 1205
2y
421 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu 440
2y
1206 GATGGTTATAGACAGAGAGGCGCTCATAGCTACACAGGGGCTCTGGCAGAGACACC 1265
2y
441 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr 460
2y
1266 GAGCACTTCGGCGCAGCTATGGAGCACAAATCCACATCATGCTCATGCTGACCAAG 1325
2y
461 GluAspPheTrpArgMetLeuTrpGluHisAsnSerThrIleValMetLeuThrLys 480
2y
1326 CTTCCGAGAGATGGCAGGGAATGCCACAGTACTGCGCAGCAGAGCGCTCTGCTCGC 1385
2y
481 LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 500
2y
1386 TACAGTACTTTGTTGATCCCGATGGCTGAGTACAACTGCCCGCATATCTCCGCT 1445
2y
501 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 520
2y
1446 GAGTTCAGGTTCAGGATGCCCGGATGGCGAGTCAAGGCAATCCGGCAGTTCCTCAGTTC 1505
2y
521 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 540
2y
1506 ACAGCTGGCCAGAGCGGCGTCCCAAGACAGCGGAGGATTCATGCTTCCTCCGGG 1565
2y
541 ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 560
2y
1566 CAGTTCATAGACACAGGACGATTTGGACGATGGCTCATCGGTCGTCAGTTCAGT 1625
2y
561 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 580
2y
1626 GCTGCGTGGCCGACCGGCGTGTTCATCTCTGAGCATCGCTCGGAGCGCATCGCC 1685
2y
581 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 600
2y
1686 TATGAGCGCTGTCGATCTTTTCAGACCGTGAAGCCCTGCGTACACAGCGTCCCTGCC 1745
2y
601 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 620
2y
1746 ATGGTGCAGACAGGACGATTCAGTGTGCTACCGTGGCGGCTGGAGTACCTCGGC 1805
2y
621 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly 640
2y
1806 AGCTTTGACCACTATGCAACG 1826
2y
641 SerPheAspHisTyrAlaThr 647

RESULT 4

AAU14379
ID AAU14379 standard; protein; 647 AA.

XX AAU14379;

XX 24-OCT-2001 (first entry)

DE Human novel protein #250.

XX Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
XX immunomodulatory; cytostatic; neuroprotective; vulnary; nootropic;
XX anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
XX antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
XX thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
XX Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
XX tissue regeneration; immune disorder.

XX Homo sapiens.

XX WO200155437-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US002623.

XX 25-JAN-2000; 2000US-00491404.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI: 2001-451939/48.

XX N-PSDB; AAS22684.

PT Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage.

XX Example 4; Page 792-793; 894pp; English.

XX The invention relates to polynucleotides encoding novel human proteins or
XX their active domains. The polypeptides, polynucleotides and antibodies
XX raised against the polypeptides are used in a method of treatment of a
XX mammal and prevention of disorders caused by the aberrant protein
XX expression or activity. The polypeptides can be used as molecular weight
XX markers, food supplements, and in antibody production. The polypeptides
XX are used to identify compounds which bind to the polypeptides.
XX Polynucleotides of the invention are used as probes and primers, for
XX sequencing, for chromosome or gene mapping, in the production of
XX recombinant proteins, and in generating anti-sense DNA or RNA and in gene
XX therapy. Polypeptides of the invention can be used to target drugs to a
XX tumour, in assays to determine biological activity, to raise
XX antibodies/ elicit an immune response, to determine quantitative protein
XX levels, as tissue markers, and to isolate receptors or ligands.
XX Polypeptides of the invention may also be useful in treating platelet
XX disorders, stem cell disorders, regenerating bone, cartilage, tendon,
XX ligament and/or nerve tissue, wound healing, treating burns, promoting
XX the proliferation, differentiation and survival of stem cells, as a
XX contraceptive, treating osteoporosis and osteoarthritis, anaemia,
XX Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
XX sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
XX fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
XX versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
XX diseases, nervous system disorders, and infection. The present sequence
XX represents a protein of the invention

XX Sequence 647 AA;

Alignment Scores:

Pred. No.:	0	Length:	647
Score:	607.00	Matches:	607
Percent Similarity:	100.00%	Conservative:	0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 53.34% Indels: 0
 DB: 4 Gaps: 0

US-09-719-272-1 (1-3467) x AAU14379 (1-647)

6 GGACTGAAGGACTCCTTCTGGCCCACTCTCTGACCTGTGGAGATCGCGAGCTCAAC 65
 41 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgLeuAsn 60
 66 TACGAGACCCAGGTATCGAGACACCCACCCTCCATCCATCCAGCTGGCGGCAAC 125
 61 TyrGlnThrProGlyMetArgAspHisProProPheProIleThrAspLeuAlaAspAsn 80
 126 ATCGAGCCCTCAAAGCAAAGTGGCTCAAGTCTCTCCAGGAGTATGATCCATCGAC 185
 81 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAsp 100
 186 CTGGACAGCAGTTCACGTGGAGAAATCAACCTCGAGGTGAACAAGCCCAAGAACCCG 245
 101 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 120
 246 TATCGGAATGTCATCGCTACGACCACTCTCGAGTCACTCTTACTCTATCGATGGCGTC 305
 121 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 140
 306 CCGGGAGTGACTACATCAATGCCAACTACATCGATGGCTACCGCAAGCAGAGTGCCTAC 365
 141 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 160
 366 ATCGCAGCAGCGGCCCTCCCGAGACCACTGGCGGATTTCTGGAGAATGGTGTGGAA 425
 161 IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheThrArgMetValTrpGlu 180
 426 CAGCGCAGCGGCACCTGTGTATGATGATGATGATGATGATGATGATGATGATGATG 485
 181 GlnArgThrAlaThrValValMetMetThrArgLeuGluLysSerArgValLysCys 200
 486 GATCAGTACTGCGCAGCGGTGGACCGGACCTGTGGCTTATTCAGTGCACCTGTG 545
 201 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 220
 546 GACACAGTGGAGCTGGCCACATACACTGTGGCCACCTTCGCACCTCCACAAGAGTGGCTCC 605
 221 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 240
 606 AGTGAAGCGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 665
 241 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 260
 666 GAGTACCCCAACTCCATCTCTGGCTTCTTACGACCGGTCAAGGCTGCAACCCCTAGAC 725
 261 GluTyrProThrProIleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAsp 280
 726 GCAGGCGCCATGTTGTGCACTGCGAGCGGGCGGTGGCGCGGCTGCTGCTGCTGCTGCT 785
 281 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 300
 786 ATTGATGCCATGTTGAGCGGATGAAGCAGCAGAGACGCTGACATCTATGGCCACCGTG 845
 301 IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisVal 320
 846 ACTGATCGGATCAACAGAGAACTACTGTTGTCAGACCGGAGACGAGTACGTGTTGTC 905
 321 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 340
 906 CATGAGCGCTGTGGAGGTGCCAGTGGCGCCACACAGAGTGGCTCCCGCAACCTG 965
 341 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 360
 966 TATGCCCACTCCAGAGCTGGCGCCCAAGTGCCTCCAGGGAGAGTGTACCGCCATGGAG 1025
 361 TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMetGlu 380

1026 CTCAGATTCAAGTTGCTGGCCAGCTCCAAAGGCCACACGCTCCCGCTTCATCAGCGCCAAC 1085
 381 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 400
 1086 CTGCCCTGCAACAGTTCAAGAACCGCTGGTGAACATCATGCTCCCTACGATTCAGATTCACCGGT 1145
 401 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 420
 1146 GTGTCTCTGCAAGCCCATCCGTGGTGTGGAGGGCTCTGACTACATCAATGCCAGTTCCTGT 1205
 421 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu 440
 1206 GATGTTATAGACACAGACGCTTACATGCTACACAGGGGCTCTGGCAGAGAGACAC 1265
 441 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr 460
 1266 GAGGACTTCTGGCGCATGCTATGGAGACCAATTCACCATCATGCTCATGCTGACCAAG 1325
 461 GluAspPheTrpArgMetLeuTrpGluHisAsnSerThrIleIleValMetLeuThrLys 480
 1326 CTTCGGAGATGGGAGGAGAAATGCCACAGTACTGGCCAGCAGAGCGCTGCTGCTGCG 1385
 481 LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 500
 1386 TACCAGTACTTTGTTGACCCGATGCTGCTGAGTACAAATGCCCCAGTATATCTGCGT 1445
 501 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 520
 1446 GAGTTCAGGTCAAGATCCCGGATCCCGGATGGCGAGTCAAGACCAATCCGCGAGTCCAGTTC 1505
 521 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 540
 1506 ACAGCTGCGCCAGAGCAGCGGCTGCCAAGACAGCGAGGGATTCATTGACTTCATTCGGG 1565
 541 ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 560
 1566 CAGGTGCATTAAGACCAAGAGCAGTTTGGACAGATGGCGCTTATCAGGTGCAGTGCAGT 1625
 561 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 580
 1626 GCTGGGTGGCGCGCAGCGGCTGCTCATCTCTGAGCATGCTCTGGAGCGCATGCGC 1685
 581 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 600
 1686 TATGAGGGCTGGTGCACATGTTTTCAGACCGTGAAGACCTCGTACACAGCGCTGCTGCG 1745
 601 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 620
 1746 ATGCTGCAGACAGACACGATCATGCTGTGCTACCGTGGCGGCTGAGTACCTCGC 1805
 621 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly 640
 1806 AGCTTTGACCACTATGCAACG 1826
 641 SerPheAspHisTyrAlaThr 647

RESULT 5

AAE37971
 ID AAE37971 standard; protein; 1796 AA.
 AC AAE37971;

XX 06-NOV-2003 (first entry)

DE Human kinase and phosphatase (KPP-16) protein.

XX Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis;
 KW atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer;
 KW psoriasis; thrombocytopenia; developmental disorder; Reiter's syndrome;
 KW renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease;
 KW neurological disorder; parkinson's disease; epilepsy; glomerulonephritis;
 KW autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome;

acquired immune deficiency syndrome; immunosuppressive; Crohn's disease; neutropenic; dermatitis; multiple sclerosis; diabetes mellitus; allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome; osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological; gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.

Homo sapiens.

WO2003050084-A2.

19-JUN-2003.

06-DEC-2002; 2002WO-US039126.

07-DEC-2001; 2001US-0340235P.

19-DEC-2001; 2001US-0343007P.

21-DEC-2001; 2001US-0343546P.

04-FEB-2002; 2002US-0354388P.

15-FEB-2002; 2002US-0357675P.

(INCY-) INCYTE GENOMICS INC.

Kable AE, Chien D, Wilson AD, Swarnakar A, Gorvad AB;

Hafalia AJA, Emerling BM, Ramkumar J, Jin P, Griffin JA, Marquis JP;

Baughn MR, Chawla NK, Lehr-Mason PM, Khare R, Lee S, Hawkins PR;

Becha SD, Lee SY, Sprague WW, Zebajradian Y;

WPI; 2003-532894/50.

N-PSDB; AAD57343.

New human kinases and phosphatases and polynucleotides, useful for

diagnosing, treating or preventing autoimmune or inflammatory disorders

(e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,

cancer or hepatitis.

Claim 1; Page 216-220; 282pp; English.

The invention relates to an isolated polypeptide, which is a human kinase

and phosphatase (KPP). KPP agonists and antagonists are useful for

diagnosing, treating or preventing disorders associated with aberrant

expression of KPP, particularly cell proliferative disorders (e.g.

arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal

nocturnal haemoglobinuria, polycythaemia vera, poriasis, primary

thrombocytopaenia or cancer), developmental disorders (eg. renal tubular

acidosis, anaemia or mental retardation), neurological disorders (e.g.

Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/

inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome,

allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's

disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,

gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome,

multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's

syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,

bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP

is useful in assessing the effects of exogenous compounds on the

expression of nucleic acids and kinases and phosphatases. KPP gene is

useful in gene therapy and for creating transgenic animals to model human

disease. The present sequence is human KPP protein

QY 66 TACGAGACCCAGGTATGGAGACACACCCATCCCATCCAGGAGGACAC 125
Db 1210 TyrGlnThrProGlyMetArgAspHisProPheProIleProIleThrAspLeuAlaAspAsn 1229
QY 126 ATGAGCGCTCAAAACCAACGATGCGCTCAAGTCTCCAGGATGATGATCCATCGAC 185
Db 1230 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAsp 1249
QY 186 CTGGAGCAGAGTTTACGTGGGAGAAATTCAACTCGAGGTGACCAAGCCCAAGACCCG 245
Db 1250 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 1269
QY 246 TATGCGAATGTCATCGCTACGACCACTCTCGAGTCACTTACCTTACCTCTCTCGATGGCTC 305
Db 1270 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 1289
QY 306 CCGGAGTCACTACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 365
Db 1290 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 1309
QY 366 ATGCGCAGCAGGCGCCCTGCGCGAGACCATGCGGATTTCTGGAGAAATGGTGGAA 425
Db 1310 IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheIleArgMetValTrpGlu 1329
QY 426 CAGCGCAGCGCCCACTGTGTGTCATGATGACACCGCTCGAGGAGAGTCCCGGTAAATGT 485
Db 1330 GlnArgThrAlaThrValValMetMetThrArgLeuGluLysSerArgValLysCys 1349
QY 486 GATCAGTACTGGCGCGCGCTGCGCGAGACCTGCGCTTATTCAGGTGACCTGTG 545
Db 1350 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 1369
QY 546 GACACAGTGGAGCTGGCCACATACATCACTGTGCGACCTTCCACTCCCAAGAGTGGCTCC 605
Db 1370 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 1389
QY 606 AGTGAGAGCGTGGCTGCTCAGTTTCACTTCACTGCGCTGCGCGACCATGAGTTCTCT 665
Db 1390 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaIleProAspHisGlyValPro 1409
QY 666 GAGTACCCAACTCCCATCTCCCTGCGCTTCTTACGAGCGGTCAAGGCTGCAACCCCTAGAC 725
Db 1410 GluTyrProThrProIleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAsp 1429
QY 726 CGAGCGGCCCATGFGTGTGCTGCTGCGCGCGGTGGCGCGCGCTGCTGCTGCTGCTGCTG 785
Db 1430 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 1449
QY 786 ATTGATGCTGATGTTGGAGCGGATGAGACGAGACGAGGAGGAGGAGGAGGAGGAGGAGG 845
Db 1450 IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisVal 1469
QY 846 ACCTGCGATGCGATCAGAGGAACTATGATGTCAGACGAGGAGGAGGAGGAGGAGGAGGAG 905
Db 1470 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 1489
QY 906 CATGAGCGCTGCTGGAGGCTGCCACGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 965
Db 1490 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 1509
QY 966 TATGCCACATCCAGAGCTGGCCCAAGTGCCTCCAGGAGGAGGAGGAGGAGGAGGAGGAG 1025
Db 1510 TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMetGlu 1529
QY 1026 CTCGAGTTCAAGTTGCTGGCGGAGCTCCAGCGCCACACGCTCCCGCTTCATCAGCGCCCAAC 1085
Db 1530 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 1549
QY 1086 GTGCGCTGCAACAAAGTTCAAGAACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1145
Db 1550 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 1569

Alignment Scores:

pred. No.:	0	Length:	1796
Score:	607.00	Matches:	607
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	53.34%	Indels:	0
JB:	6	Gaps:	0

US-09-719-272-1 (1-3467) x AAE37971 (1-1796)

2y 6 GGACTGAGGACTCTGCTGGCCCACTCTCTGACCTCTGAGGTGGAGGCTCAAC 65

Db 1190 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgLeuAsn 1209

QY 1146 GTGTGCTGAGCCCATCGTGTGTGGGGCTCTGACTACATCAATGCGACCTTCCTG 1205
Db 1570 ValCysLeuGlnProIleAsglyValGluGlySerAspTyrIleAenAlaSerPheLeu 1589
QY 1206 CATGTTATAGACAGAGAGGCTCATAGCTACACAGGGCTCTGGCAGAGACACC 1265
Db 1590 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr 1609
QY 1266 GAGACTTCTGGCCATGCTATGGAGACAAATCCACCATCATCGTCATGCTGACCAAG 1325
Db 1610 GluAspPheTrpArgMetLeuTrpGluHisAenSerThrIleValMetLeuThrLys 1629
QY 1326 CTTCCGAGAGTGGCAGGAGAAATGCCAGTACTGGCAGCAGAGCCCTCTGTCGC 1385
Db 1630 LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 1649
QY 1386 TACAGACTTGTGTTGATGCCCATGCTGAGTACACATGCCAGTATATCTTCCTGCGT 1445
Db 1650 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 1669
QY 1446 GAGTTCAGAGTCAAGGTCAGGATGCCCGGATGGGAGTCAAGGACAATCCGGCAGTTC 1505
Db 1670 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleAsgGlnPhe 1689
QY 1506 ACAGACTGGCAGAGAGGGCTGCCAGACAGGCGAGGATTCTATGACTTCATCGGG 1565
Db 1690 ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 1709
QY 1566 CAGGTGCATAGACCAAGAGCAGTTCGACAGATGGGCTATCAGCGTGCACTGCAGT 1625
Db 1710 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1729
QY 1626 GCTGGCGTGGCCGACCGGGTGTTCATCTGATCATCTGAGCATCGCTCGGAGCGATCGC 1685
Db 1730 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 1749
QY 1686 TATGAGGCGTGTGCGACATGTTTCAGACCGTGAAGACCTGCGTACACAGCGTCTGCGC 1745
Db 1750 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuAsgThrGlnArgProAla 1769
QY 1746 ATGTTGCAGACAGAGCACAGTATCAGTGTGCTACCTGCGGCGCTGAGTACTCGGC 1805
Db 1770 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly 1789
QY 1806 AGCTTTGACCATATGCCAAG 1826
Db 1790 SerPheAspHisTyrAlaThr 1796
RESULT 6
AAY81785
ID AAY81785 standard; protein; 1897 AA.
XX AC AAY81785;
XX DT 07-JUN-2000 (first entry)
XX Human protein tyrosine phosphatase, LAR, protein sequence.
XX DE
XX Human; protein tyrosine phosphatase; antibody; intracellular domain; LAR;
XX KW CD45; PTP; diagnosis; insulin resistance related disease; syndrome X;
XX KW non-insulin dependent diabetes mellitus; arteriosclerosis; therapy;
XX KW heart disorder.
XX OS Homo sapiens.
XX PN WO200002922-A1.
XX PD 20-JAN-2000.
XX PF 06-JUL-1999; 99WO-JP003656.
XX PR 10-JUL-1998; 98WO-JP003120.
XX

(FUSO) FUSO PHARM IND LTD.
XX Yamamoto H, Tsujikawa K, Uchino Y;
XX WPI; 2000-182215/16.
XX N-PSDB; AAZ91908.
XX Antibody for diagnosis and treatment of insulin resistance disorders and
XX syndrome X recognises the intracellular domains of tyrosine kinases.
XX Example 1; Page 61-77; 83pp; Japanese.
XX This sequence is the protein tyrosine phosphatase LAR. The invention
XX relates to an antibody specifically recognising the intracellular domains
XX of two or more protein tyrosine phosphatases (PTP). The antibody is
XX useful for the detection and assay of PTP including novel phosphatases
XX generated by cloning; and diagnosis, treatment and prevention of insulin
XX resistance related diseases and non-insulin dependent diabetes mellitus,
XX syndrome X and arteriosclerosis and heart disorders
XX
SQ Sequence 1897 AA;
Alignment Scores:
Pred. No.: 0 Length: 1897
Score: 607.00 Matches: 607
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.34% Indels: 0
DB: Gaps: 0
US-09-719-272-1 (1-3467) x AAY81785 (1-1897)
QY 6 GGACTGAAGGACTCTGTGCTGCCCATCTCTGTGACCTGTGGAGATCGGAGGCTCAAC 65
Db 1291 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgArgLeuAen 1310
QY 66 TACAGACCCAGGTATGCGAGACACACCCATCCCATCCAGCTGGCGGAGAAC 125
Db 1311 TyrGlnThrProGlyMetArgAspHisProIleThrAspLeuAlaAspAen 1330
QY 126 ATCGAGCGCTCAAGCAACAGTGCCTCAAGTTCCTCCAGGAGTATGAGTCCATCCAC 185
Db 1331 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGlyTyrGluSerIleAsp 1350
QY 186 CTTGGACAGCAGTTCACGTGGGAGAAATCAAACTGGAGGTGAACAAGCCAGAACCGC 245
Db 1351 ProGlyGlnGlnPheThrTrpGluAsnSerAenLeuGluValAsnLysProLysAenArg 1370
QY 246 TATGCAATGTCTATCGCTTACGACCATCTCTGAGTCATCTTACCTCTATCGATGGCGTC 305
Db 1371 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 1390
QY 306 CCGGAGTGAATCAATCAATGCCAACTACATCGATGGCTACCCAGCAGAGAAATGCTTAC 365
Db 1391 ProGlySerAspTyrIleAsnAlaAenTyrIleAspGlyTyrArgLysGlnAlaTyr 1410
QY 366 ATGCGCAGCAGGCGCCCTGCGGAGACCATGGCGATTTCTGGAGATGTGTGGGAA 425
Db 1411 IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGlu 1430
QY 426 CAGCGACAGCGCCACTGCTGCTATGATGACACCGCTGGAGGAGAGTCCCGGTAAATGT 485
Db 1431 GlnArgThrAlaThrValValMetMetThrArgLeuGluLysSerArgValLysCys 1450
QY 486 GATCAGTACTGGCCAGCGCTGGCAGCAGCTGTGGCTTATTCAGGTGACCTGTGTG 545
Db 1451 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 1470
QY 546 GACACAGTGGAGTGGCCACATACACTGTGCGCACCTTCGCTACTCCACAGAGTGGCTCC 605
Db 1471 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 1490
QY 606 AGTGAGAGCGGTGAGCTGGCTGCTGCTTTCATGCTTCATGGCTGCCAGACCATGGAGTTCCT 665

1491 SerGluYArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 1510
666 GAGTACCAACTCCATCCCTGCGCTTCCTACGAGCGGTCAAGCGCTGCAACCCCTAGAC 725
1511 GluTy-ProThrProIleLeuAlaPheLeuArgValValAlaCysAsnProLeuAsp 1530
726 GCAGGCGCATGGTGTGCACTCAGCGGGGGTGGCGGACCGGCTGCTTCATCGTG 785
1531 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 1550
786 ATGATGCCATGTTGAGCGGATGAAGACGAGACGAGCGGTGACATCTATGCCACGTG 845
1551 IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleTyGlyHisVal 1570
846 ACCTGATCGATCAGACGAGAACTCATGGTGCACACGAGGAGGACGACGTGTTTCATC 905
1571 ThrCysMetArgSerGlnArgAsnTyMetValGlnThrGluAspGlnTyValPheIle 1590
906 CATGAGCGCTGCTGGAGGCTGCCACGTGGCCACACAGAGTGCTGCCCGCAACCTG 965
1591 HisGluAlaLeuLeuGluAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 1610
966 TATGCCCATCAGACGAGCTGGCCAGTGGCTCCAGGGGAGGTGACCGCCATGGAG 1025
1611 TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMetGlu 1630
1026 CTCGAGTTCAAGTTGCTGGCGAGCTCCAGCGCCACACGCTCCCGCTTCATCAGCGCAAC 1085
1631 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 1650
1086 CTGCGCTGCAACAGTTCAAGACCGCTGGTGAACATCATGCTCATCATGCTTCCTG 1145
1651 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyGluLeuThrArg 1670
1146 GTGTGCTGTCAGCCCATCGCTGTGTGGAGGCTCTGACTACATCATGCTCATGCTTCCTG 1205
1671 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyIleAsnAlaSerPheLeu 1690
1206 GATGGTTATAGACAGAGAGGCTCATAGCTACACAGGGCTCTGGCAGAGACAC 1265
1691 AspGlyTyArgGlnGlnLysAlaTyIleAlaThrGlnGlyProLeuAlaGluSerThr 1710
1266 GAGGACTTCTGGCGCATGCTATGGAGACAAATCCACCATCATGCTCATGCTGACCAAG 1325
1711 GluAspPheIleArgMetLeuTrpGluHisAsnSerThrIleIleValMetLeuThrLys 1730
1326 CTTCCGAGATGGCAGGAGAAATGCCACGATCTGCGCAGCAGAGCGCTCTGCTGCG 1385
1731 LeuArgGluMetGlyArgGluLysCysHisGlnTyTrpProAlaGluArgSerAlaArg 1750
1386 TACCAGTACTTGTGTGTCGCGTGGTGGTACACATGCCAGTATATCTCTGCGT 1445
1751 TyrGlnTyPheValValAspProMetAlaGluTyTrpAsnMetProGlnTyIleLeuArg 1770
1446 GAGTTCAAGTTCAGGATGCCCGGATGGCAGTCAAGGACAAATCCCGGCTGCTCAGTTC 1505
1771 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1790
1506 ACAGCTGGCCAGACAGCGGCTGCCAACAGCGGAGGATTCATTGACTTCATCGGG 1565
1791 ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 1810
1566 CAGGTGCATAGACCAAGGAGCAGTTTGGACGAGATGGGCTTATCAGGTGCACTGCAGT 1625
1811 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1830
1626 GCTGGGTGGCCGACCGGGGTGTTTATCTCTGAGCATCTGCTGGAGCGCATGCGC 1685
1831 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 1850
1686 TATCAGGCGGTGGTGCATGTTTCAGACCGTGAAGACCGCTGCGTACACAGCGCTCTGCC 1745

1851 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 1870
1746 ATGCTGCAGACAGAGGACCACTATCAGCTGTGTACGTCGCGCTGAGTACCTCGGC 1805
1871 MetValGlnThrGluAspGlnTyGlnLeuCysTyArgAlaLeuGluTyLeuGly 1890
1806 AGCTTTCACCACTATGCAACG 1826
1891 SerPheAspHisTyAlaThr 1897
RESULT 7
AAY56100
ID AAY56100 standard; protein; 1897 AA.
XX AAY56100;
XX 17-APR-2000 (first entry)
XX LAR tyrosine phosphatase.
XX Intracellular domain; P-subunit; human; leucocyte antigen related; LAR;
XX tyrosine phosphatase; antibody; thyroid cancer.
XX Homo sapiens.
XX WO9964591-Al.
XX 16-DEC-1999.
XX 07-JUN-1999; 99WO-JP003054.
XX 08-JUN-1998; 98WO-JP002542.
XX (FUSO) FUSO PHARM IND LTD.
XX Yamamoto H, Tsujikawa K, Uchino Y, Konishi N;
XX WPI; 2000-097539/08.
XX N-PSDB; AAZ59133.
XX Antibody recognizing the intracellular domain of the human tyrosine
XX phosphatase LAR.
XX Disclosure; Page 81-97; 104pp; Japanese.
XX This sequence represents the complete human leucocyte antigen related
XX (LAR) tyrosine phosphatase. The invention relates to the generation of an
XX antibody recognizing the intracellular domain of the human LAR tyrosine
XX phosphatase (AAY56098). The antibody is used for the diagnosis and
XX treatment of thyroid cancer
XX
XX Sequence 1897 AA;
Alignment Scores:
Pred. No.: 0 Length: 1897
Score: 607.00 Matches: 607
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.34% Indels: 0
DB: 3 Gaps: 0
US-09-719-272-1 (1-3467) x AAY56100 (1-1897)
QY 6 GAGCTGAGAGGACTCTTCTGCTGCGCCACTCTCTGACCCCTGTGGAGATCCGAGGCTCAAC 65
DB 1291 GlyLeuLysAspSerLeuAlaHisSerSerAspProValGluMetArgLeuAsn 1310
QY 66 TACCAGACCCAGAGTATCGGAGACACCCACCCATCCCATCCAGCTCGGCGGACAAAC 125
DB 1311 TyrGlnThrProGlyMetArgAspHisProIleThrAspLeuAlaAspAsn 1330
QY 126 ATCGAGCGCTCAAGACCAACGATGGGCTCAAGTTCCTCCAGGAGTATGATCCATCGAC 185

1331 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAsp 1350
186 CCTGGACAGCAGTTCACGTGGAGAAATCAACCTGGAGGTGAACAGCCAGACCCG 245
1351 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 1370
246 TATCGAATGTCATCGCTACGACCACTCTCGAGTCATCTTACCTCTATCGATGGCGTC 305
1371 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 1390
306 CCGGGAGTGATCATCAATGCGCAACTACATCATGCTACCGCAAGCAAGATGCTTAC 365
1391 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 1410
366 ATCGCCAGCAGGCGCCCTCCCGAGACCACTGGCGATTCTTCGAGAAATGGTGGCAA 425
1411 IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheThrArgMetValTrpGlu 1430
426 CAGCGACGGCCATGCTGTCATGATGACACGGCTGGAGGAGAGTCCCGGGTAAATGT 485
1431 GlnArgThrAlaThrValValMetMetThrArgLeuGluGluLysSerArgValLysCys 1450
486 GATCAGTACTGGCCAGCGCTGGCCAGACCTGTGGCTTATTCAGGTGACCTGTG 545
1451 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 1470
546 GACACAGTGGAGCTGSCCAGATACACTGTGGCACTTCGCACATCCCAAGAGTGGCTCC 605
1471 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 1490
606 AGTGAGAGCGTGAGCTGGCTCAGTTTCAGTTTCAGTCTGGCTGGCCAGACCATGGAGTTCCT 665
1491 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaIleProAspHisGlyValPro 1510
666 GAGTACCACTCCCATCTCTGCGCTCTTACGACGGGTCAAGCGCTGCAACCCCTAGAC 725
1511 GluTyrProThrProIleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAsp 1530
726 GAGGGCCCATGGTGTGTCACGTGACCGCGGCTGGCGCCAGCGCTGTTCATCGTG 785
1531 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 1550
786 ATTGATGCATCTGGAGCGGTGAAGCAGCAGAGAGCGGTGGACATCTATGGCCAGCTG 845
1551 IleAspAlaMetLeuGluArgMetLysHisGlyLysThrValAspIleTyrGlyHisVal 1570
846 ACTGCATCGCATCAGAGAACTACATGTGTGACGAGCGGAGGACCATGTGTTCTATC 905
1571 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 1590
906 CATGAGGCGCTCTGAGGCTCCAGCTGGCGCCACACAGAGTGCCTCCCGCCAGCAACCTG 965
1591 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 1610
966 TATGCCCATCATCAGAACTGGGCCAAGTGTCTCCAGGGGAGAGTGTACCGCCATGGAG 1025
1611 TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMetGlu 1630
1026 CTCGAGTTCAGTGTGCTGCGCTCCAGGCGCCACAGCTCCCGTTCATCAGCGCCCAAC 1085
1631 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 1650
1086 CTGCCCTGCAACAAGTTCAGAACCGGCTGGTGAACATCATCCCTACGAATGACCGCT 1145
1651 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 1670
1146 GTGTGTCTGAGCCCATCGTGTGTGGAGGCTCTGACTACATCAATGCCAGTTCCTG 1205
1671 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu 1690
1206 GATGGTTATAGACAGCAGAGGCTTACATAGCTTACACAGGGCGCTCTGCGCAGAGACCC 1265
1691 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr 1710

QY 1266 GAGGACTTCTGGCGCATGCTATGGAGCACAATTCACCATCATCGTCATGCTACCAAG 1325
Db 1711 GluAspPheThrArgMetLeuTrpGluHisAsnSerThrIleIleValMetLeuThrLys 1730
QY 1326 CTTCCGGAGATGGGAGAGAAATGCCAGTACTGGCCAGCAGAGCGCTCTGCTCGC 1385
Db 1731 LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 1750
QY 1386 TACCAGTACTTGTGTGGTACCCGATGGCTCAGTACACATGCCCAAGTATATCTCGCT 1445
Db 1751 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 1770
QY 1446 GAGTTCAAGGTCACGATGCCCGGATGGCGAGTCAGTCAGGACAATCCGGCAGTTCAGTTC 1505
Db 1771 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1790
QY 1506 ACAGACTGGCCAGACAGCGGGTGGCCCAAGACAGCAGGAGGATTCAATGACTTTCATCGG 1565
Db 1791 ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 1810
QY 1566 CAGGTGTCATAGACCAAGGAGCAGTTTCGACAGGATGGGCTTATCACGGTGCATGCACT 1625
Db 1811 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1830
QY 1626 GCTGGCTGGCGCGCAGCGGGTGTTCATCTCTGAGCATCGTCTCGAGCGCATGCGC 1685
Db 1831 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 1850
QY 1686 TATGAGGGCGTGGTCGACATGTTTCAGACCGTGAAGACCTCGGTACACAGCGTCTGCC 1745
Db 1851 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 1870
QY 1746 ATGTGTCAGACAGAGACCATGATCAGCTGTGCTACCGTGGCGGCTCGAGTACCTCGC 1805
Db 1871 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaLeuGluTyrLeuGly 1890
QY 1806 AGCTTTGACCACTATGCCAAGC 1826
Db 1891 SerPheAspHisTyrAlaThr 1897
RESULT 8
AAB19712
ID AAB19712 standard; protein; 1897 AA.
XX AC AAB19712;
XX DT 19-FEB-2001 (first entry)
XX DE Human protein tyrosine phosphatase PAP LAR.
XX KW PTP LAR; protein tyrosine phosphatase; leukocyte antigen related; human; epithelial cell; cell migration; cell proliferation; cancer; antitumour; metastasis; antimetastatic; wound healing; vulnery; diagnosis; therapy.
XX OS Homo sapiens.
XX FH Key
XX FT Peptide 1..16 /label= Signal_peptide
XX FT Protein 17..1897 /label= Mature_protein
XX FT Domain 37..99 /label= Immunoglobulin_domain
XX FT Domain 139..199 /label= Immunoglobulin_domain
XX FT Domain 236..290 /label= Immunoglobulin_domain
XX FT Domain 309..391 /label= Fibronectin-type-III_domain
XX FT Domain 403..490 /label= Fibronectin-type-III_domain
XX FT Domain 502..584

T Domain /label= Fibronectin-type-III_domain
 T 596..696
 T /label= Fibronectin-type-III_domain
 T 698..799
 T /label= Fibronectin-type-III_domain
 T 811..894
 T /label= Fibronectin-type-III_domain
 T 905..990
 T /label= Fibronectin-type-III_domain
 T 1365..1596
 T /label= Protein-tyrosine_phosphatase

T WO20061180-A2.

X 19-OCT-2000.

X 06-APR-2000; 2000WO-US009274.

X 09-APR-1999; 99US-0128673P.

X (PLAC) MAX PLANCK INST.

X Ullrich A, Muller T;

X WPI; 2000-647399/62.

X N-PSDB; AAA88739.

T Treating a disease or a disorder characterized by epithelial cell
 T migration comprises administering a pharmaceutically acceptable
 T composition comprising PTP LAR.

X Disclosure; Fig 9; 107pp; English.

X The present sequence is that of human protein tyrosine phosphatase PTP
 X LAR (leukocyte antigen related), a negative regulator of epithelial cell
 X migration and tumour formation, for which beta-catenin is a substrate. A
 X dysfunction of PTP LAR may lead to tumour invasion and metastasis. The
 X invention provides methods for diagnosing, preventing, or treating a
 X disease or disorder characterized by epithelial cell migration, increased
 X tyrosine phosphorylation of beta-catenin, and/or increased levels of the
 X pool of free beta-catenin, especially cancer, metastasis and aberrant
 X wound healing (claimed). The methods may also be used to treat diseases
 X and disorders with abnormal cell proliferative conditions, including
 X fibrotic and mesangial disorders, abnormal angiogenesis and
 X vasculogenesis, psoriasis, diabetes mellitus and inflammation. Methods
 X are provided for identifying compounds that modulate PTP LAR activity for
 X use in treatment

X Sequence 1897 AA;

X Alignment Scores:

Pred. No.: 0 Length: 1897
 Score: 607.00 Matches: 607
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 53.34% Indels: 0
 DB: 3 Gaps: 0

US-09-719-272-1 (1-3467) x AAB19712 (1-1897)

QY 6 GGACTGAAGNCTCTTGCTGGCCCACTCTCTGACCTCTGGAGATGCGAGGCTCAAC 65
 Db 1291 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgArgLeuAsn 1310
 QY 66 TACCAGACCCAGATGATGCGAGACACCCACCCATCCCGACCTGGCGGCAAC 125
 Db 1311 TyrGlnThrProGlyMetArgAspHisProProlleProIleThrAspLeuAlaAspAsn 1330
 QY 126 ATCAGAGCCCTCAAGCCACGATGGCTGAGTCTCCAGGAGTATGATCCATCGAC 185
 Db 1331 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAsp 1350
 QY 186 CTGGACAGCAGTTCACGTGGGAGATTCAAACCTGGAGGTGAACAGCCCAAGACCCG 245

Db 1351 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 1370
 QY 246 TATGCGAATGTCTATCGCTACGACCACTCTCGAGTCACTCTACCTCTCTATCGATGCGCTC 305
 Db 1371 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 1390
 QY 306 CCGGGAGTGACTACATCAATGCAATCACTCATCGATGGCTACCGCAAGCAGATGCTCTAC 365
 Db 1391 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 1410
 QY 366 ATGCGCACGCGAGGCGCCCTGCGGAGACCACTGGGAGATTCCTGGAGAATGGTGTGGGAA 425
 Db 1411 IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGlu 1430
 QY 426 CAGCGCACGCGCACTGTGTGATGACACGCGCTGGAGAGAGTCCCGGGTAAATGT 485
 Db 1431 GlnArgThrAlaThrValValMetMetThrArgLeuGluGluLysSerArgValLysCys 1450
 QY 486 GATCAGTACTGGCGAGCCCTGCGCAGCACTGTGGCTTATTCAGGTGACCTGTGTG 545
 Db 1451 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 1470
 QY 546 GACACAGTGGAGTGGCCACATACATCTGTGCGCACTTCGCACTCCACAGAGTGGCTCC 605
 Db 1471 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 1490
 QY 606 AGTGAGAGGTGAGTGGCTGCTCAGTTTCAGTTCATGCGCTGGCCGACACCATGAGTTCCT 665
 Db 1491 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaIleTrpProAspHisGlyValPro 1510
 QY 666 GAGTACCCCACTCCCATCTCGGCTTCTCTACGAGGGTCAAGGCTCGCAACCCCTAGAC 725
 Db 1511 GluTyrProThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp 1530
 QY 726 CGAGGCGCCATGTTGGTGGCTGCTGCTGCGCGGGTGGCGCGCCGCTGCTTCATCGTG 785
 Db 1531 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 1550
 QY 786 ATTGATGCGATTTGGAGCGGATGAAGCAGAGAGACGGTGGACATCTATGCGCCAGTG 845
 Db 1551 IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisVal 1570
 QY 846 ACCTGCTATGCGATCAGAGAGAACTATCATGTTGACAGCGAGGACCGATGCTGCTTATC 905
 Db 1571 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 1590
 QY 906 CATGAGCGCTGCTGGAGGCTGCCACGTGGCGCCACACAGAGGTGCTGCCCGCAACCTG 965
 Db 1591 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 1610
 QY 966 TATGCCCATCCAGAACTGGCCAAAGTGGCTCCAGGGAGAGTGTACCGCCATGAG 1025
 Db 1611 TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMetGlu 1630
 QY 1026 CTCGAGTTCAAGTTCGTCGCGCAGCTCCAAAGCCACACAGCTCCCGCTTCATCAGCGCCAAC 1085
 Db 1631 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 1650
 QY 1086 CTGCGCTGCCAACAAAGTTCAGAACCGCTGTGTGACATCATGCGCTCAGATTCACCGCT 1145
 Db 1651 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 1670
 QY 1146 GGTGCTCTGCGCCCATCCGTTGGTGGAGGGCTCTGACTACATCAATGCCAGTCTCTCTG 1205
 Db 1671 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu 1690
 QY 1206 GATGTTTATAGACAGCAGAGGCGCTTACATAGCTACACAGGGCGCTCTGGCAGAGACCC 1265
 Db 1691 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr 1710
 QY 1266 GAGGACTTCTGGCGATCTATGGAGCAGCATCCACCATCGTCTCATCTGACCAAG 1325

Db 1711 GluAspPheTrpArgMetLeuTrpGluHisAsnSerThrIleValMetLeuThrLys 1730
Qy 1326 CTTGGAGATGGCAGGAGAAATGCCACAGTACTGGCCACAGAGCGCTGCTGCGC 1385
Pt |||||
Db 1731 LeuArgGluMetGlyA:gglyuCyHisGlnTrpProAlaGluArgSerAlaArg 1750
Qy 1386 TACCAGTACTTTGTTGTTGACCCCATGGCTGAGTACACATGCCGCCAGTATATCTCGGT 1445
Ps |||||
Db 1751 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 1770
Qy 1446 GAGTTCAAGTACAGATGCCCGGATGGGAGTCAAGGACATCCCGGAGTTCAGTTC 1505
Db 1771 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1790
Qy 1506 ACAGACTGCCAGACAGCGCGCTGCTGCCAAGACAGCGGAGGATTCATTGACTTCATCGGG 1565
Db 1791 ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 1810
Qy 1566 CAGGTGCATAGACACAGACAGTTCGACAGATGGGCTATCAGGTGCAGTGCAGT 1625
Db 1811 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1830
Qy 1626 GCTGCGTGGCGCGCACCGGCTGTTCATCTCTGAGCATCGTCTCGAGCGCATCGGC 1685
Db 1831 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 1850
Qy 1686 TATGAGCGGTGGTCGACATGTTTCAGACCGTGAAGCCCTGCGTACACAGCGTCTGCC 1745
Db 1851 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 1870
Qy 1746 ATGGTGCAGACAGAGGACAGTATCAGTGTGCTACCGTGGCGGCTCGGAGTACCTCGGC 1805
Db 1871 MetValGlnThrGluAspGlnTyrGlnLeuGlyCysTyrArgAlaAlaLeuGluTyrLeuGly 1890
Qy 1806 AGCTTTGACCACTATGCAACG 1826
Db 1891 SerPheAspHisTyrAlaThr 1897
RESULT 9
ADD18740
ID ADD18740 standard; protein; 1897 AA.
AC ADD18740;
DT 15-JAN-2004 (first entry)
DE Human disease related protein SeqID171.
XX human; disease state; cytostatic; antiinflammatory; ophthalmological;
KW antiarteriosclerotic; vulnary; gene therapy;
KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
KW glucose transport; catecholamine synthesis; iron transport;
KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
KW inflammatory condition; wound healing.
XX Homo sapiens.
OS
XX
XX WO2003018621-A2.
PN
XX
PD 06-MAR-2003.
XX
XX 23-AUG-2002; 2002WO-GB003892.
PF
XX
XX 23-AUG-2001; 2001GB-00020558.
PR
XX
XX 05-OCT-2001; 2001GB-00024037.
PR
XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
PA
XX
XX Kingman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
PI
XX
XX WPI; 2003-290046/28.
XX

DR N-PSDB; ADD18741.
XX New substantially purified polypeptide, useful for diagnosing or treating
Pt a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
Pt injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
Pt wound healing.
XX Claim 25; SEQ ID NO 171; 424pp; English.
PS
XX This invention relates to novel human genes and gene product which are
XX implicated in certain disease states. Compounds which modulate the
CC proteins of the invention may have cytostatic, antiinflammatory, the
CC ophthalmological, antiarteriosclerotic or vulnary activities. The
CC sequences of the invention may be useful for gene therapy. The invention
CC may be useful for diagnosing or treating a hypoxia-regulated condition,
CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
CC erythropoiesis, or the biological response to hypoxia conditions
CC including processes such as glycolysis, gluconeogenesis, glucose
CC transport, catecholamine synthesis, iron transport or nitric oxide
CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
CC inflammatory conditions or wound healing. The present sequence is that of
CC a disease related protein of the invention.
XX
XX Sequence 1897 AA;

Alignment Scores:
Pred. No.: 0 Length: 1897
Score: 607.00 Matches: 607
Percent Similarity: 100.00% Conservations: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.34% Indels: 0
DB: 7 Gaps: 0

US-09-719-272-1 (1-3467) x ADD18740 (1-1897)

Qy 6 GGACTGAAGGACTCTCTGCTGCTGCCCATCTCTGACCTGTGGAGATGGGAGCTCAAC 65
Db 1291 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgArgLeuAsn 1310
Qy 66 TACCAGACCCAGGTATGGAGACACCCACCATCCCTCCCATCACCAGCTGGCGGACAAAC 125
Db 1311 TyrGlnThrProGlyMetArgAspHisProProlleThrAspLeuAlaAspAsn 1330
Qy 126 ATGAGCGCTCAAGCCCAACGATGGCTCAAGTTCTCCAGAGATGATGATGCTCATGAC 185
Db 1331 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAsp 1350
Qy 186 CTTGGACAGCAGTTCACGTGGGAGATTCACAACTGAGGCTGCAACAAGCCCAAGAACCGC 245
Db 1351 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 1370
Qy 246 TATGCGAATGTCTATCGCTTACGACCACTCTCGAGTCACTCTTACCTTATCGATGGCTC 305
Db 1371 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 1390
Qy 306 CCGGGAGTGACTACTCATCATCATCCACTCATCGTGTGCTACCGCAAGCAGAGATGCTCTAC 365
Db 1391 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 1410
Qy 366 ATGCCACGACGAGGCGCCCTCCCGGAGACCATGGCGGATTTCTGGAGATGTTGGGAA 425
Db 1411 IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGlu 1430
Qy 426 CAGGCGACGCGCTCTGTGTCATGATGACACCGCTGGAGGAGAGTCCCGGTAAATCT 485
Db 1431 GlnArgThrAlaThrValMetMetThrArgLeuGluGluLysSerArgValLysCys 1450
Qy 486 GATCAGTACTGCGCAGCCCGTGGCAGACCTGTGGCTTATTTCAGGTGACCTGTTG 545
Db 1451 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 1470
Qy 546 GACACGTGAGCTGGCCACATACATCTGTGGCACCTTGGCACTCCACAGAGTGGCTCC 605

1471	AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer	1490
606	AGTGAAGAAGCGTGAGCTCGCTCAGTTTCAGTTTCATCGCTGGCCGGCCACACCATGAGTTCCT	665
1491	SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro	1510
666	GAGTACCCAACTCCCATCTCCGCTTCCTACGACGGGTCAAGCCCTGCACCCCTAGAC	725
1511	GluTyrProThrProIleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAsp	1530
726	GCAGGCGCCATGCTGTGTGCATCTCAGCGCGGGCTGGCGCGCACCGCTCTTCATCGTG	785
1531	AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal	1550
786	ATTGATGCCATGTTGGAGCGGATGAAGCAGCAGAACCGGTGGACATCTATGCGCCACGTG	845
1551	IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisVal	1570
846	ACCTGCATCGATCAGACGAGGAACACTACATGCTGCACGCGGAGCACCAGTACGTGTTCAAC	905
1571	ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle	1590
906	CATGAGCGCTGCTGGAGCGCTGCACGCTGGCGGCCACACAGAGGTGCTGCCGCCAACCTG	965
1591	HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu	1610
966	TATGCCCATCTCAGAAGCTGGGCCAAGTCCCTCCAGGGGAGAGTGTGACCGCATGGAG	1025
1611	TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGlnSerValThrAlaMetGlu	1630
1026	CTCGAGTTCAAGTTGCTGGCCAGCTCCAAAGGCCACACAGTCCCGCTTCATCAGCGCCAAC	1085
1631	LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn	1650
1086	CTCGCTGCAACAAAGTTCAAGAACCGGCTGCTGTAACATCATGCTCCCTACGATGACCCGT	1145
1651	LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg	1670
1146	GTCTGTCTGCAGCCCATCGCTGTGTGGAGGCTCTGACTACATCAATCAATGCACCTTCCTG	1205
1671	ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu	1690
1206	GATGGTTATAGACAGCAAGAAGCCTACATAGCTACACAGGGGCTCTGGCAGAGACACC	1265
1691	AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr	1710
1266	GAGGACTTCTGGCGCATGCTATGGGACCAATTCACCATCATCTGCTACGTGTCAGCAAG	1325
1711	GluAspPheTrpArgMetLeuTrpGluHisAsnSerThrIleIleValMetLeuThrLys	1730
1326	CTTCGGAGATGGCAGGAGAAATGCCACAGTACTGGCGCAGCAGACGCCCTCTGCTCGC	1385
1731	LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg	1750
1386	TACAGTACTTTGTTGTTGACCCGATGGCTGAGTACAACATGCCCCAGTATATCTTCGCT	1445
1751	TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg	1770
1446	GAGTTCAAGTTCACGATGCCCGGATGGCGAGTCAAGGACAATCCGGCAGTTTCCAGTTC	1505
1771	GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe	1790
1506	ACAGCTGGCCAGACGAGGCGTGCCTCCCAAGCAGGCGAGGATTCATATGATTCATCGGG	1565
1791	ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly	1810
1566	CAGTGCATTAAGACCAAGGACGATTGGACAGATGGGCTATCAGGTGCACTGCAGT	1625
1811	GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer	1830
1626	GCTGGCGTGGCCGCACCGGGGTGTTTCATCACTCTGACATCTGCTGGAGCGCATGCCG	1685

Db	1931	AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg	1895
Qy	1686	TATCAGGGCGTGGTCGACATGTTTTCAGACCGTGAAGACCTCGGTACACAGCGTCTCTGCC	1745
Db	1851	Tyr-GluGlyValValAspMetPheGlnThrValIleThrLeuArgThrGlnArgProAla	1870
Qy	1746	ATGGTGCAGACAGACAGACAGTATCAGCTGTGCTACCGTGCAGCCCTGGAGTAGTACCTCGGC	1805
Db	1871	MetValGlnThrGluAspGlnIleThrGlnLeuGlyArgAlaAlaLeuGluIleLeuGly	1890
Qy	1806	AGCTTTTACCACCTATGCAACG	1826
Db	1891	SerPheAspHisTyrAlaThr	1897
RESULT 10			
AAU14143			
XX	ID	AAU14143 standard; protein; 1907 AA.	
XX	AC	AAU14143;	
XX	DT	24-OCT-2001 (first entry)	
XX	XX	Human novel protein #14.	
DE	XX	Human; novel protein; Antianaemic; osteopathic; antiinflammatory;	
KW	XX	immunomodulatory; cytostatic; neuroprotective; vulnery; nootropic;	
KW	XX	anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;	
KW	XX	antibacterial; antiatheric; dermatological; haemostatic; antiasthmatic;	
KW	XX	thrombolytic; immunogen; antibody; gene therapy; neurological disorder;	
KW	XX	Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;	
KW	XX	tissue regeneration; immune disorder.	
OS	XX	Homo sapiens.	
XX	XX	WO200155437-A2.	
PN	XX	02-AUG-2001.	
XX	PD		
XX	PF	25-JAN-2001; 2001WO-US002623.	
XX	XX	25-JAN-2000; 2000US-00491404.	
PR	XX	(HYSE-) HYSEQ INC.	
PA	XX		
PI	XX	Tang YT, Liu C, Drmanac RT;	
PI	XX	WPI; 2001-451939/48.	
DR	XX	N-PSDB; AAS22448.	
XX	XX		
PT	XX	Isolated polypeptides useful for treating anti-inflammatory diseases,	
PT	XX	nervous system disorders, and for regenerating bone and cartilage.	
XX	XX	Example 4; Page 533-537; 894pp; English.	
PS	XX	The invention relates to polynucleotides encoding novel human proteins or	
XX	XX	their active domains. The polypeptides, polynucleotides and antibodies	
CC	XX	raised against the polypeptides are used in a method of treatment of a	
CC	XX	mammal and prevention of disorders caused by the aberrant protein	
CC	XX	expression or activity. The polypeptides can be used as molecular weight	
CC	XX	markers, food supplements, and in antibody production. The polypeptides	
CC	XX	are used to identify compounds which bind to the polypeptides.	
CC	XX	Polynucleotides of the invention are used as probes and primers, for	
CC	XX	sequencing, for chromosome or gene mapping, in the production of	
CC	XX	recombinant proteins, and in generating anti-sense DNA or RNA and in gene	
CC	XX	therapy. Polypeptides of the invention can be used to target drugs to a	
CC	XX	tumour, in assays to determine biological activity, to raise	
CC	XX	antibodies/elicit an immune response, to determine quantitative	
CC	XX	levels, as tissue markers, and to isolate receptors or ligands.	
CC	XX	Polypeptides of the invention may also be useful in treating platelet	
CC	XX	disorders, stem cell disorders, regenerating bone, cartilage, tendon,	
CC	XX	ligament and/or nerve tissue, wound healing, treating burns, promoting	
CC	XX	the proliferation, differentiation and survival of stem cells, as a	
CC	XX	contraceptive, treating osteoporosis and osteoarthritis, anaemia,	

CC Alzheimer's, Parkinson's and Huntington's diseases, amyloidotic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma, graft-
 CC versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory
 CC diseases, nervous system disorders, and infection. The present sequence
 CC represents a protein of the invention
 XX
 SQ Sequence 1907 AA;

Alignment Scores:
 Pred. No.: 0 Length: 1907
 Score: 607.00 Matches: 607
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 53.34% Indels: 0
 DB: 4 Gaps: 0

US-09-719-272-1 (1-3467) x AAU14143 (1-1907)

QY 6 GGACTGAAGGACTCCTTGTGTCGCCCACTCTCTGACCTGTGGAGATGCGGAGCTCAAC 65
 Db 1301 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgArgLeuAsn 1320

QY 66 TACGACAGCCAGGATGCGGAGACACACCCCACTCCCATCAGGACCTGCGGAGCAAC 125
 Db 1321 TyrGlnThrProGlyMetArgAspHisProProlIleThrAspLeuAlaAspAsn 1340

QY 126 ATCGAGCGCTCAAGCAACGATCGCTCAAGTTCTCCAGGAGTATGATCCATCGAC 185
 Db 1341 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAsp 1360

QY 186 CTGACAGCAGCTTACGTGGAGATTCMAACCTGGAGGTGACACAGCCCAAGACCGC 245
 Db 1361 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProGlyAsnArg 1380

QY 246 TATGGGAATGTATCGCTTACGACCACTCTCGAGTCATCTTACCTCTATCGATGGCGTC 305
 Db 1381 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 1400

QY 306 CCGGGAGTGACTATCATATCCAACTACATCGATGCTACCGGACGACAGCAATGCCTAC 365
 Db 1401 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAlaTyr 1420

QY 366 ATCGCCACGACGCGCCCTGCGGAGACCAATGGCGATTTCTGGAGAAATGGTGGGAA 425
 Db 1421 IleAlaThrGlnGlyProLeuProGlnThrMetGlyAspPheTrpArgMetValTrpGlu 1440

QY 426 CAGCGCACGCGCCACTGTGTCTATGATGACACGCGTGGAGAGATCCCGGTTAAATGT 485
 Db 1441 GlnArgThrAlaThrValValMetMetThrArgLeuGluGluLysSerArgValLysCys 1460

QY 486 GATCAGTACTGCGCCGCGTGGCCAGACCTGTGGCTTATTTCAGTGACCTGTGTG 545
 Db 1461 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 1480

QY 546 GACACAGTGGAGTGGCCATACACTGTGCGACCTTGGCACTCCACAGAGTGGCTCC 605
 Db 1481 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 1500

QY 606 AGTGAGACGCTGAGCTGCTCAGTTTCAGTTTCATGGCTGGCCGACCATGGAGTTCCT 665
 Db 1501 SerGluLysArgGlnLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 1520

QY 666 GAGTACCCAACTCCCACTCTGGCTTCTTACGACGGTCAAGCTCGAACCCCTAGAC 725
 Db 1521 GluTyrProThrProlIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp 1540

QY 726 GCAGGCGCCATGTGTGTGACTGACGCGGGCGGTGGCGCGGCTGCTTCATCTCG 785
 Db 1541 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 1560

QY 786 ATTGATGCCATGTGGAGCGGATGAAGACGAGACGCTGACATCTATGGCCACGTCG 845

Db 1561 IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisVal 1580

QY 846 ACTGTCATGCGATCACAGAGAACTACATGTGTGACAGCGAGGACCACTGCTGTTCATC 905

Db 1581 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 1600

QY 906 CATGAGCGCTGCTGAGGCTGCCACGTGCGGCGCACACAGAGGTGCTGCCGCGCACTG 965

Db 1601 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 1620

QY 966 TATGCCCATCCAGAGCTGGCCCAAGTCTCCAGGGGAGAGTGTACCGCCATGAG 1025

Db 1621 TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMetGlu 1640

QY 1026 CTCGAGTTCAAGTTCTGCTGCCAGCTCCAAAGGCCACACGTCCTGTTTCATCAGCGCCAAC 1085

Db 1641 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 1660

QY 1086 CTGCCCTGCAACAAGTTCAAGAACCGGTGGTGAACATCATGCCCTCAGAAATGACCGT 1145

Db 1661 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 1680

QY 1146 GTGTGTCTGCAGCCCATCCGTGTGTGAGGGCTCTGACTACATCAATGCGCAGCTTCCTG 1205

Db 1681 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu 1700

QY 1206 GATGTTATAGACAGCAGAGGCTTACATAGCTACACAGGGGCTCTGCGAGAGACACC 1265

Db 1701 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr 1720

QY 1266 GAGGACTTCTGCGCATGCTATGGGAGCACAAATTCACCATCATCGTCATGTCGACCAAG 1325

Db 1721 GluAspPheTrpArgMetLeuTrpGluHisAsnSerThrIleIleValMetLeuThrLys 1740

QY 1326 CTTCGGGAGATGGCAGGAGGAAATGCCACCACTACTGCGCAGCAGAGCGCTCTCTCGC 1385

Db 1741 LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 1760

QY 1386 TACCACTATTGTGTTGTTTACCCCGATGCTGAGTACAAATGCCCCAGTATCTCTCGT 1445

Db 1761 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 1780

QY 1446 GAGTTCAGATCCGATCCCGGATGGGCGAGTCAAGACAAATCGGCAGTCCAGTTC 1505

Db 1781 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1800

QY 1506 ACAGATGCGCCAGCAGCGCGTGGCCCAAGACAGCGAGGAGTTCATTGACTTCATCGGG 1565

Db 1801 ThrAspTrpProGlnGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 1820

QY 1566 CAGGTGCATAAGACCAAGAGCAGATTGTGACAGGATGGGCTTATCAGGTGCTGCACTG 1625

Db 1821 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1840

QY 1626 GCTGGGTGGCGCGCACCGGGTGTTCATCCTCTGAGCATCTCTGAGCGGCGATCGCC 1685

Db 1841 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 1860

QY 1686 TATGAGGCGCTGCTGCACATGTTTCAGACCGTGAAGACCTCGGTACACAGCGTCTCGCC 1745

Db 1861 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 1880

QY 1746 ATGGTGCAGACAGAGCCAGTATCAGCTGTGCTACCGTGGCGGCTGAGTACCTCGGC 1805

Db 1881 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly 1900

QY 1806 AGCTTTGACCACTATGCAACG 1826

Db 1901 SerPheAspHisTyrAlaThr 1907

RESULT 11
 AAB56372
 ID AAB56372 standard; protein; 442 AA.

CX AAB56372;
 AC 13-MAR-2001 (first entry)
 CX Human prostate cancer antigen protein sequence SEQ ID NO:950.
 DE
 CX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 CW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
 CW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;
 CW antibacterial; gene therapy; neural; immune; reproductive; renal;
 CW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 CW wound; infectious disease.
 CX Homo sapiens.
 DS
 CX WO200055174-A1.
 PN 21-SEP-2000.
 CX 08-MAR-2000; 2000WO-US005988.
 CX 12-MAR-1999; 99US-0124270P.
 CX (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 CX Rosen CA, Ruben SM;
 PI WPI, 2000-587513/55.
 CX N-PSDB; AAF15575.
 DR
 CX Prostate cancer associated gene sequences, referred to as prostate cancer
 PT antigens, useful for treatment, prevention, and diagnosis of disorders
 PT such as prostate cancer.
 CX Claim 11; Page 1389-1390; 2338pp; English.
 PS AAF15566 to AAF16505 encode the human prostate cancer associated
 CX proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
 CC The prostate cancer antigens can have neuroprotective, cytostatic,
 CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,
 CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
 CC and can be used in gene therapy. The prostate cancer antigen
 CC polynucleotides may be used for detection of prostate cancer, chromosome
 CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The prostate cancer antigens may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 CC AAB57303 represent sequences used in the exemplification of the present
 CC invention
 CX
 CX Sequence 442 AA;
 SQ
 Alignment Scores:
 Pred. No.: 0 Length: 442
 Score: 442.00 Matches: 442
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 38.84% Indels: 0
 DB: 3 Gaps: 0
 US-09-719-272-1 (1-3467) x AAB56372 (1-442)
 QY 501 GCCGTGGCAGCAGACTGGCCCTTATTCAGGTGACCTGTGGACACAGTGGAGCTG 560
 DB 1 AlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeuAspThrValGluLeu 20
 QY 561 GCACATACACTGTCGACACCTTCACCTCCACAGAGTGGCTCCAGTGAGAGCGTGAG 620
 DB 21 AlaThrTyThrValArgThrPheAlaLeuHisSerGlySerGlySerGlyArgGlu 40

QY 621 CTGGCTCAGTTTCAGTTTCATGGCTGGCCAGACCATGGAGTTCCTGAGTACCAACTCCC 680
 DB 41 LeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGluTyProThrPro 60
 QY 681 ATCTGGCCCTTCCTACACCGGCTCAGGCTGCAACCCCTAGCAGGAGGCCCATGGTG 740
 DB 61 IleLeuAlaPheLeuArgValValLysAlaCysAsnProLeuAspAlaGlyProMetVal 80
 QY 741 GTGCACCTGCAGCGGGCGGGCGCCGACCGGCTGCTTCATCGTATGATGATGATGATG 800
 DB 81 ValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeu 100
 QY 801 GAGCGGTGAACACGAGAACGCGTGGACATCATATGCGCACGTCGACCTGCGATCA 860
 DB 101 GluArgMetLysHisGluLysThrValAspIleTyGlyHisValThrCysMetArgSer 120
 QY 861 CAGAGGAACATGCTGTCAGACCGGAGGACGACGTCGTTCATCCATGAGGGCGCTGCTG 920
 DB 121 GlnArgAsnTyMetValGlnThrGluAspGlnTyValPheIleHisGluAlaLeuLeu 140
 QY 921 GAGGCTGCCACGTCGCGCCACACAGAGTGGCTCCCGCCCAACCTGTATGCCCATCCAG 980
 DB 141 GluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeuTyAlaHisIleGln 160
 QY 981 AAGCTGGCCCAAGTGCCTCCAGGGGAGAGTGTGACCGCCATGGAGCTCGAGTCAAGTTG 1040
 DB 161 LysLeuGlyGlnValProProGlyLysValThrAlaMetGluLeuGluPheLysLeu 180
 QY 1041 CTGGCCAGCTCCAAAGGCCACACGCTCCCGCTTCATCAGCGCCCAACCTGCCCTCAACAAG 1100
 DB 181 LeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLys 200
 QY 1101 TTCAGAACCCGGCTGGTGAACATCATGCCCTACGATTCAGATTCACCGCTGTGCTCCAGCCC 1160
 DB 201 PheLysAsnArgLeuValAsnIleMetProTyGluLeuThrArgValCysLeuGlnPro 220
 QY 1161 ATCCGTGTGTGGAGGGCTCTGACTACATCAATGCAGCTTCCTGGTGGTGTATAGACAG 1220
 DB 221 IleArgGlyValGluGlySerAspTyIleAsnAlaSerPheLeuAspGlyTyArgGln 240
 QY 1221 CAGAGGCTCATAGCTACAGGGGCTCTGGCAGAGACCGAGGACTTCTGGGCGC 1280
 DB 241 GlnLysAlaTyIleAlaThrGlnGlyProLeuAlaGluSerThrGluAspPheTrpArg 260
 QY 1281 ATGCTATGGAGCAATTCACCATCATCTGCTGCTGACCAAGCTTCGGGAGATGGGC 1340
 DB 261 MetLeuTrpGluHisAsnSerThrIleIleValMetLeuThrLysLeuArgGluMetGly 280
 QY 1341 AGGGAGAAATGCCACCTACTGCGCCAGCAGCGCTCTGCTCGCTACCACTACTTTGTT 1400
 DB 281 ArgGluLysCysHisGlnTyTrpProAlaGluArgSerAlaArgTyGlnTyPheVal 300
 QY 1401 GTTGACCGATGGCTGACTACACATGCCCGCATATATCTCGTGGTTCAGGTCAAGTCAAG 1460
 DB 301 ValAspProMetAlaGluTyAsnMetProGlnTyIleLeuArgGluPheLysValThr 320
 QY 1461 GATGCCCGGGATGGGCACTCAAGGCAATCCGGCGCATTCAGTTCCAGACTGGCCAGAG 1520
 DB 321 AspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPheThrAspTrpProGlu 340
 QY 1521 CAGGGGTGCCCAACACAGCGGAGGGATTCATTCATCGGCGCAGGTGCATTAAGACC 1580
 DB 341 GlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGlnValHisLysThr 360
 QY 1581 AAGGAGCAGTTTGGACAGGATGGGCTATCAGGTGCACTGCGAGTGTGGGTGGGGCGCC 1640
 DB 361 LysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSerAlaGlyValGlyArg 380
 QY 1641 ACCGGGTGTTTCATCCTCTGAGCATCTGCTCGGAGCGCATGCGCTATGAGGGCGGTGTC 1700
 DB 381 ThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArgTyGluGlyValVal 400
 QY 1701 GACATGTTTTCAGACCGTGAAGACCCTGGGTACACAGCGCTCTGCTGCCATGCTGTCAGACAG 1760

Db 401 AspMetPheGlnThrValIleThrLeuArgThrGlnArgProAlaMetValGlnThrGlu 420
QY 1761 GACCAGTATCAGCTGTGCTACCGTGGCCCTGGAGTACCTCGGACGCTTTGACCACTAT 1820
Db 421 AspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGlySerPheAspHisTyr 440
QY 1821 GCACG 1826
Db 441 AlaThr 442
RESULT 12
ABM78984
ID ABM78984 standard; protein; 296 AA.
XX AC ABM78984;
XX 15-JAN-2004 (first entry)
XX Human leukocyte common antigen related protein.
XX DE Human; leukocyte common antigen related protein; LAR;
XX KW protein tyrosine phosphatase; enzyme.
XX OS Homo sapiens.
XX WO2003073987-A2.
XX PD 12-SEP-2003.
XX 26-FEB-2003; 2003WO-US005950.
XX PF New 3,5 dibromo-4-hydroxybenzene carbonyl benzofuran derivatives
XX PR inhibiting protein tyrosine phosphatase and T-cell protein tyrosine
XX PT phosphatase are useful to treat e.g. type 2 diabetes, inflammation and
XX PT immune system disorders.
XX PA (SUNE-) SUNESIS PHARM INC.
XX PI Barr K, Fahr B, Hansen S, Wiesmann C;
XX DR WPI; 2003-756750/71.
XX PT New 3,5 dibromo-4-hydroxybenzene carbonyl benzofuran derivatives
XX PT inhibiting protein tyrosine phosphatase and T-cell protein tyrosine
XX PT phosphatase are useful to treat e.g. type 2 diabetes, inflammation and
XX PT immune system disorders.
XX PS Disclosure; Fig 7; 58pp; English.
XX CC The present sequence is the protein sequence of human protein tyrosine
XX CC phosphatase leukocyte common antigen related protein (LAR). The invention
XX CC provides novel 3,5-dibromo-4-hydroxybenzene carbonyl benzofuran
XX CC derivatives that modulate the activity of human protein tyrosine
XX CC phosphatase 1B (PTP-1B, see ABM78982) by binding to a novel binding site,
XX CC termed the exosite, that is distal to the PTP-1B active site. These
XX CC compounds do not inhibit LAR, in which the exosite-forming residues of
XX CC PTP-1B are generally not conserved. The compounds are useful for treating
XX CC diabetes and/or its associated complications such as insulin resistance
XX CC and obesity
XX SQ Sequence 296 AA;
Alignment Scores:
Pred. No.: 4,98e-274 Length: 296
Score: 296.00 Matches: 296
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.01% Indels: 0
Gaps: 0
DB:
US-09-719-272-1 (1-3467) x ABM78984 (1-296)
QY 102 CCATCAGCAGCTGGCGGACACATCGAGCGCTCAAAGCCAAAGCTGCGCTCAAGTTC 161

Db 1 ProIleThrAspLeuAlaAspAsnIleGluArgLeuLysAlaAsnAspGlyLeuLysPhe 20
QY 162 TCCAGGAGTATGAGTCCATCCAGCCCTCGACAGAGTTTCAGTGGGAGAAATCAAACTG 221
Db 21 SerGlnGluTyrGluSerIleAspProGlyGlnGlnPheThrTrpGluAsnSerAsnLeu 40
QY 222 GAGGTGAACACAGCCCAAGAACCGCTATCGAATGTGCATCGCTACGACCACTCTCGAGTC 281
Db 41 GluValAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAspHisSerArgVal 60
QY 282 ATCTTACCTCTATCGATGGGTCCCGGGAGTGAATCATCAATGCCAATCATCATCAT 341
Db 61 IleLeuThrSerIleAspGlyValProGlySerAspTyrIleAsnAlaAsnTyrIleAsp 80
QY 342 GGTACCGCAGCAGAAATGCCTACATCGCCAGCGAGGCCCCCTCCCGGACCACTGGGC 401
Db 81 GlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGlyProLeuProGluThrMetGly 100
QY 402 GATTTCTGAGAAATGGTGGGAAACAGCGCAGCGGCACTGTGGTGCATGATGACACGGCTG 461
Db 101 AspPheTrpArgMetValTrpGluGlnArgThrAlaThrValValMetMetThrArgLeu 120
QY 462 GAGGAGAGTCCCGGTAAATGTGATCAGTACTGCCAGCCGCGTGGCAGCAGCACTGT 521
Db 121 GluLysSerArgValLysCysAspGlnTyrTrpProAlaArgGlyThrGluThrCys 140
QY 522 GGCCTTATTGAGTGACCTGTGTGACACAGTGGAGTGGCCACATACACTGTGGCCACC 581
Db 141 GlyLeuIleGlnValThrLeuLeuAspThrValGluLeuAlaThrTyrThrValArgThr 160
QY 582 TTCGCACCTCCACAAGAGTGGCTCCAGTGAGAGCGGTGAGTCCGTGAGTTTCAGTTTCATG 641
Db 161 PheAlaLeuHisLysSerGlySerSerGluLysArgGluLeuArgGlnPheGlnPheMet 180
QY 642 GCCTGCCACAGCAGTACCTGCTGAGTACCACCACTCCCATCTGGCTTCTCTACAGCG 701
Db 181 AlaTrpProAspHisGlyValProGluTyrProThrProIleLeuAlaPheLeuArgArg 200
QY 702 GTCAGGCGCTGCACACCCCTAGACGAGGCGCCATGGTGGTGCCTGACGCGCGGCGCTG 761
Db 201 ValLysAlaCysAsnProLeuAspAlaGlyProMetValValHisCysSerAlaGlyVal 220
QY 762 GCGCGCACCGCTGCTTCATCGTGTATGATGATGATGATGATGATGATGATGATGATGATG 821
Db 221 GlyArgThrGlyCysPheIleValIleAspAlaMetLeuGluArgMetLysHisGluLys 240
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QY 882 ACGGAGGACGACGATCGTGTTCATCCATGAGGCGCTGCTGGAGGCTGCCACGTCGCGCCAC 941
Db 261 ThrGluAspGlnTyrValPheIleHisGluAlaLeuLeuGluAlaAlaThrCysGlyHis 280
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AAG78268
ID AAG78268 standard; protein; 306 AA.
XX AC AAG78268;
XX 19-DEC-2001 (first entry)
XX DE Human DCA-D1.
XX KW PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;
XX KW dephosphorylation; phosphotyrosine; human; PTP1b; mouse; fruit fly;
XX OS Homo sapiens.

XX FN WO200161031-A2.
XX KD 23-AUG-2001.
XX PR 13-FEB-2001; 2001WO-US005180.
XX PR 14-FEB-2000; 2000US-0181769P.
XX PA (CEPT-) CEPTYR INC.
XX PT Flint AJ, Cool DE;
XX PT WPI; 2001-570570/64.
XX PR Screening assays to identify agents that alter protein tyrosine
XX PT phosphatase (PTP) binding to, and PTP-mediated catalytic
XX PT dephosphorylation of phosphotyrosine peptide substrates.
XX PR Disclosure; Fig 1; 79pp; English.
XX CC The invention relates to identifying agents which alter the interaction
XX CC between a protein tyrosine phosphatase (PTP) and a tyrosine
XX CC phosphorylated polypeptide using fluorescence energy signals. The methods
XX CC are useful for performing screening assay to identify agents that alter
XX CC PTP binding to and PTP-mediated catalytic dephosphorylation of
XX CC phosphotyrosine peptide substrates. The present sequence is that of a
XX CC catalytic domain of a PTP for comparison with human PTPB (AAG78262)
XX CC
XX CC Sequence 306 AA;
XX CC
XX CC Alignment Scores:
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XX CC DB: 4 Gaps: 0
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XX CC 255 GTCATCGCTACGACCTCCGAGTTCATCTACCTCTATCGATGCGTCCCGGGAGT 314
XX CC 21 ValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyValProGlySer 40
XX CC 315 GACTACATCAATGCCAACTACATCGATGGTACCGCAAGCAGAGATGCTACATCGCCACG 374
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ID AAG78287 standard; protein; 294 AA.
XX AC AAG78287;
XX DT 19-DEC-2001 (first entry)
XX DE Human BCA-D2.
XX PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;
XX KW dephosphorylation; phosphotyrosine; human; PTPB; mouse; fruit fly;
XX KW yeast.
XX OS Homo sapiens.
XX XX WO200161031-A2.
XX PD 23-AUG-2001.
XX PF 13-FEB-2001; 2001WO-US005180.
XX PR 14-FEB-2000; 2000US-0181769P.
XX PA (CEPT-) CEPTYR INC.
XX PI Flint AJ, Cool DE;
XX DR WPI; 2001-570570/64.
XX Screening assays to identify agents that alter protein tyrosine
XX PT phosphatase (PTP) binding to, and PTP-mediated catalytic
XX PT dephosphorylation of phosphotyrosine peptide substrates.
XX PS Disclosure; Fig 1; 79pp; English.
XX CC The invention relates to identifying agents which alter the interaction
XX CC between a protein tyrosine phosphatase (PTP) and a tyrosine
XX CC phosphorylated polypeptide using fluorescence energy signals. The methods
XX CC are useful for performing screening assay to identify agents that alter
XX CC PTP binding to and PTP-mediated catalytic dephosphorylation of
XX CC phosphotyrosine peptide substrates. The present sequence is that of a
XX CC catalytic domain of a PTP for comparison with human PTPB (AAG78262)
XX CC
XX CC Sequence 294 AA;
XX CC
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Db 21 IleMetProTyrGluLeuThrArgValCysLeuGlnProIleArgGlyValGluGlySer 40
QY 1182 GACTACATCAATGCCAGCTTCTGTGATGGTTATAGACAGGAGGCTCATAGCTACA 1241
Db 41 AspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnGlnLysAlaTyrIleAlaThr 60
QY 1242 CAGGGGCTCTGGCAGACAGACCCAGGACTTCTGGCGCATCTATGGGAGCACAAATTC 1301
Db 61 GlnGlyProLeuAlaGluSerThrGluAspPheTyrArgMetLeuTyrGluHisAsnSer 80
QY 1302 ACCATCATGTCATCTGACCAAGCTTCGGAGATGGCAGGAGAAATGCCACAGTAC 1361
Db 81 ThrIleIleValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyr 100
QY 1362 TGGCCAGCAGAGCGCTCTGCTGCTGCTACCACTTCTGTGTGACCCGATGGCTGAGTAC 1421
Db 101 TrpProAlaGluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyr 120
QY 1422 AACATGCCCCAGTATATCTCGTGTGAGTTCAAGTTCACGGATGCCGGGATGGCAATCA 1481
Db 121 AsnMetProGlnTyrIleLeu-----PheLysValThrAspAlaArgAspGlyGlnSer 138
QY 1482 AGGACAATCCGGCAGTTCAGTTCCAGACTGACACTGGCCAGAGCAGGCGTCCCAACACAGGC 1541
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QY 1542 GAGGATTCATTGACTTCATCCGGCAGGTGCATAGACCAAGGAGCAGTTTGGACAGAT 1601
Db 159 GluGlyPheIleAspPheIleGlnValHisLysThrLysGluGlnPheGlyGlnAsp 178
QY 1602 GGGCTATCAGGTGCACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1661
Db 179 GlyProIleThrValHisCysSerAlaGlyValGlyArgThrGlyValPheIleThrLeu 198
QY 1662 AGCATCGTCTGGAGCGCATGCGCTATGAGGCGGTGTGCGACATGTTTCAGACCGTGAAG 1721
Db 199 SerIleValLeuGluArgMetArgTyrGluGlyValValAspMetPheGlnThrValLys 218
QY 1722 ACCCTGCTACACAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1781
Db 219 ThrLeuArgThrGlnArgProAlaMetValGlnThrGluAspGlnTyrGlnLeuCysTyr 238
QY 1782 CGTGGCGCCCTGGAGTACCTC 1802
Db 239 ArgAlaAlaLeuGluTyrLeu 245

RESULT 15
AAB59370
ID AAB59370 standard; protein; 250 AA.
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AC AAB59370;
XX
XX 21-MAR-2001 (first entry)
DE
DE Human protein tyrosine phosphatase #6.
XX
XX Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;
KW substrate trapping.
KW
XX Homo sapiens.
XX
XX WO200075339-A1.
PN
XX 14-DEC-2000.
PD
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XX
PF 24-MAY-2000; 2000WO-US014211.
XX
PR 03-JUN-1999; 99US-0137319P.
PR 16-JUN-1999; 99US-0033457S.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
XX Tonks NK, Zhang S;
XX
XX WPI; 2001-080598/09.
XX
XX New substrate trapping mutant protein tyrosine phosphatases (PTP) in
XX which the wild type PTP catalytic domain invariant apparatus is replaced
XX with an unphosphorylated amino acid, useful in gene therapy.
XX
XX Disclosure; Fig 1; 109pp; English.
XX
XX The present invention provides substrate trapping mutant protein tyrosine
XX phosphatases (PTPs). They can be used to reduce the activity of tyrosine
XX phosphorylated proteins and to screen for modulators capable of altering
XX the binding of protein tyrosine phosphatases to their substrate. These
XX may be used in disease diagnosis and treatment
XX
XX Sequence 250 AA;
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Score: 141.00 Matches: 189
Percent Similarity: 96.92% Conservative: 0
Best Local Similarity: 96.92% Mismatches: 0
Query Match: 12.39% Indels: 6
DB: 4 Gaps: 0
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QY 558 CTGGCCACATACACTGTGGCACCCTTCGCACTCCACAGAGTGGCTCCAGTGAGAGCGT 617
Db 122 LeuAlaThrTyrThrVal-----PheAlaLeuHisLysSerGlySerGluLysArg 139
QY 618 GAGCTCGCTCAGTTTCAGTTTCATGCGCTGGCCAGACCATGGAGTTCCTCAGTACCCAACT 677
Db 140 GluLeuArgGlnPheGlnPheMetAlaTyrProAspHisGlyValProGluTyrProThr 159
QY 678 CCCATCTCGCTCTCTACAGCGGTGAGGCTGCAACCCCTAGACGCGAGGCGCCATG 737
Db 160 ProIleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAspAlaGlyProMet 179
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Db 180 ValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMet 199
QY 798 TTGAGCGGATGAGCAGAGAGCGGTGGACATCTATGGCCAGTGCAGTCCCTGCTGGA 857
Db 200 LeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisValThrCysMetArg 219
QY 858 TCACAGAGGAACATACATGTCGACAGCGAGGAGGACAGTACGTGTTTCATTCATGAGCGCTG 917
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QY 918 CTGGAGGCTGCCACGTGCGGCCACACAGAGGTG 950
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240 LeuGluAlaAlaThrCysGlyHisThrGluVal 250

Search completed: March 9, 2004, 09:03:18
Job time : 205 secs

GenCore version 5.1.6
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M nucleic - protein search, using frame_plus_n2p model

Run on: March 9, 2004, 09:03:24 ; Search time 115 Seconds
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Searched: 809742 seqs, 211153259 residues

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Total number of hits satisfying chosen parameters: 1535912

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description

ALIGNMENTS

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US-10-291-265-722
Sequence 722, Application US/10291265
Publication No. US20030232054A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al
TITLE OF INVENTION: No. US20030232054A1elel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10291.265
CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 722
LENGTH: 647
TYPE: PRT

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3	442	38.8	442	9	US-09-925-300-950	Sequence 950, App
4	296	26.0	296	14	US-10-374-539-3	Sequence 3, Appl
5	296	26.0	296	15	US-10-374-499-9	Sequence 9, Appl
6	289	25.4	289	14	US-10-314-232-13	Sequence 13, Appl
7	202	17.8	306	9	US-09-788-626-8	Sequence 8, Appl
8	197	17.3	294	9	US-09-788-626-27	Sequence 27, Appl
9	52	1502	1502	10	US-09-808-602-54	Sequence 54, Appl
10	59	5.2	1502	10	US-09-800-198-44	Sequence 44, Appl
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16	29	2.5	64	14	US-10-029-386-30320	Sequence 30320, A
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34	12	1.1	248	9	US-09-848-294-10	Sequence 10, Appl
35	12	1.1	248	14	US-10-293-231-10	Sequence 10, Appl
36	12	1.1	264	14	US-10-245-539-6	Sequence 6, Appl
37	12	1.1	292	14	US-10-314-232-12	Sequence 12, Appl
38	12	1.1	309	9	US-09-788-626-11	Sequence 11, Appl
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40	12	1.1	310	9	US-09-788-626-10	Sequence 10, Appl
41	12	1.1	310	9	US-09-788-626-15	Sequence 15, Appl
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DB	161	IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheThrProMetValTyrGlu	180
QY	426	CAGCCACGCGCCTCTGTGTCATGATGACACGGCTGGAGGAGAAAGTCCCGGTAAATGT	485
DB	181	GlnArgThrAlaThrValValMetMetThrArgLeuGluLysSerArgValLysCys	200
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DB	241	SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTyrProAspHisGlyValPro	260
QY	666	GAGTACCAACTCCCATCTCTGCTCTCTAGCAGCGGTCAAGGCTGCAACCCCTAGAC	725
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QY	726	GCAGGCGCATCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	785
DB	281	AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal	300
QY	786	ATTGATGCATGTTGGAGCGGATGAGCAGCAGAGAGCGTGGATCATCTATGGCCAGCTG	845
DB	301	IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisVal	320
QY	846	ACCTGCATCGATCAGAGGAACTACATGTTGTCAGACGAGGACCACTAGCTGTTCATC	905
DB	321	ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle	340

RESULT 2

US-10-291-265-250
; Sequence 250, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)

CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 250
LENGTH: 1907
TYPE: PRT
ORGANISM: Homo sapiens
IS-10-291-265-250

Alignment Scores:
read. No.: 0 Length: 1907
Score: 607.00 Matches: 607
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.34% Indels: 0
Gaps: 0
IS-09-719-272-1 (1-3467) x US-10-291-265-250 (1-1907)
6 GGACTGAGGACTCCTTGCTGGCCCTCTCTGACCCCTGTGGAGATCGGAGGCTCAAC 65
1301 GlyLeuLysAspSerLeuLeuAlaHisSerAspProValGluMetArgLeuAsn 1320
66 TACCAGACCCAGGATGTCGAGACCAACCCACCCATCCCATCCCATCCGACCTGGCGGACAAAC 125
1321 TyrGlnThrProGlyMetArgAspHisProPheProIleThrAspLeuAlaAspAsn 1340
126 ATGAGGCGCTCAAGCAACGATGGCTCAAGTCTCCAGGAGTATGATCCATCGAC 185
1341 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluThrGluSerIleAsp 1360
186 CTTGGACAGCAGTTCACGTGGGAGAAATCAAACTGGAGGTGAACAGCCCAAGAACCGC 245
1361 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 1380
246 TATCGGAATGTATCGGCTTACGACCATCTCGAGTATCTTACCTTACCTATCGATGGCTC 305
1381 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 1400
306 CCGGGAGTGACTACATCAATGCCAATGACATGATGCTACCGCAAGCAGAGATGCTTAC 365
1401 ProGlySerAspPheIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 1420
366 ATCCGACGACGAGCCCTCTGCCGAGACCATGGCGGATTTCTGGAGATGGTGGGAA 425
1421 IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheThrArgMetValTrpGlu 1440
426 CAGGCGAGGCGCATGTGTTCATCATGACCGGTGGAGAGAGTCCCGGGTAAATGT 485
1441 GlnArgThrAlaThrValValMetMetThrArgLeuGluLysSerArgValLysCys 1460
486 GATCAGTACTGGCCAGCCGCTGGCAGCCAGACCTGTGGCTTATTCAGGTGACCCCTGTG 545
1461 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 1480
546 GACACAGTGGAGCTGGCCACATACATGCTGGCGACCTTCGACTCCACAGAGTGGCTCC 605
1481 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 1500
606 AGTCAGAACGCTGAGCTCGCTCAGTTTCAGTTTCAGTTCATGGCTGGCCAGACCATGGAGTTCCCT 665
1501 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 1520
666 GAGTACCCCACTCCCATCCTCGCTTCTCTACGAGGGTCAAGGCTCGACCCCTAGAC 725

1521 GluTyrProThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp 1540
726 GCAGGCGCCATGTGTGTGCTACTCAGCGGGGGCTGGCGGACCGGCTCTCATCGTG 785
1541 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 1560
786 ATTGATCCCATGTTGGAGCGGATGAAGACAGACGAGACCGGTGGACATCTATGGCCACGTG 845
1561 IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisVal 1580
846 ACCTGCATGCGATCACAGAGAACTACATGGTCCACACGAGGACACGATGATGTTCTATC 905
1581 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 1600
906 CATGAGCGCTGCTGAGGCTGCCAGTGGGGCCACACAGAGGTGCTGCCGCCAACCTG 965
1601 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 1620
966 TATCCCATCCAGAAAGCTGGGCCAAGTCCCTCCAGGGGAGAGTGTGACCGCATGGAG 1025
1621 TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMetGlu 1640
1026 CTCGAGTTCAGTGTGCTGGCCAGCTCCAGGCCCCACACGCTCCCGCTTCATCAGCGCCAAAC 1085
1641 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 1660
1086 CTGCGCTCAACAAAGTTCAGAAACCGGCTGGTGAACATCATGCTCCCTACGAATTGACCCGT 1145
1661 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 1680
1146 GTGTGCTGACGACCCATCCGTGGTGGAGGGCTCTGACATCATCATCATGTCAGCTTCTCTG 1205
1681 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu 1700
1206 GATGTTATACACAGCAGAAAGCTTACATAGCTACACAGGGGCTCTGGCAGAGACACC 1265
1701 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr 1720
1266 GAGACTTCTGGCCATGCTATGGAGCACAATTCACCATCATCATGCTCATGCTGACCAAG 1325
1721 GluAspPheThrArgMetLeuTrpGluHisAsnSerThrIleIleValMetLeuThrLys 1740
1326 CTTCCGAGATGGGCGAGGAGAAATGCCAGTACTGGCCAGCAGAGCGCTCTGCTCGC 1385
1741 LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 1760
1386 TACCACTTCTGTTGTTGACCCGATGCTGAGTACAAACATGCCCGCCAGTATATCTCGGT 1445
1761 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 1780
1446 GAGTTCAGAGTCCAGGATGCCGGATGGGCGAGTCAAGGACAAATCCGCGAGTTCAGTTC 1505
1781 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1800
1506 ACAGACTGCGCAGAGCAGGCGTCCCAAGACAGCGGAGGAGTTCATTGACTTATCGGG 1565
1801 ThrAspTrpProGlnGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 1820
1566 CAGGTGCATAGACCAAGCAGCAGTGGAGCAGATGGCCCTATCAGGTGCATCTGCACT 1625
1821 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1840
1626 GCTGCGTGGGCGCCAGCCGGGTGTTCATCATCTGAGCATCTGCTGGAGCGCATGCGC 1685
1841 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 1860
1686 TATGAGGCGGTGTCGATGTTTCAGACCGCTGAGACCTCGCTGACACGCGCTCGGCC 1745
1861 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGluArgProAla 1880
1746 ATGGTGCACAGACAGGACCATGATCATGCTGCTGCTGCGGCGCTGGAGTACTCGGC 1805

Db 1881 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaLeuGluTyrLeuGly 1900
2y 1806 AGCTTTCACCATATGCAACG 1826
Db 1901 SerPheAspHisTyrAlaThr 1907

RESULT 3
US-09-925-300-950
Sequence 950, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 950
LENGTH: 442
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-300-950

Alignment Scores:
Pred. No.: 0 Length: 442
Score: 442.00 Matches: 442
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 38.84% Indels: 0
DB: 9 Gaps: 0

US-09-719-272-1 (1-3467) x US-09-925-300-950 (1-442)

QY 501 GCCGTGACACGAGCTGGCTTATTCAGTGGACCCCTGGACACAGTGGAGCTG 560
Db 1 AlaArgGlyThrGluThrCysGlyLeuGlnValThrLeuLeuAspThrValGluLeu 20
QY 561 GCACATACACTGTCCGACCTTCGACCTCCACAGAGTGGCTCCAGTGAGAACGCTGAG 620
Db 21 AlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySerGluLysArgGlu 40
QY 621 CTGCTCAGTTTCAGTTTCAGTGGCCGACACCATGAGTTCCTGAGTACCCCACTCCC 680
Db 41 LeuArgGlnPheGlnPheMetAlaThrProAspHisGlyValProGluTyrProThrPro 60
QY 681 ATCTCTGGCCTTCTACGACGGGTCAAGGCTGCAACCCCTAGACGCGAGGCCCATGGTG 740
Db 61 IleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAspAlaGlyProMetVal 80
QY 741 GTGCACTGAGCGGGCGTGGCGCGACCGCTCTTCATGATGATGATGATGATGATG 800
Db 81 ValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeu 100
QY 801 GAGCGATCAAGCACGAGAGCGGTGGACATCTATGGCCAGCTGACCTGCATGCGATCA 860
Db 101 GluArgMetLysHisGluLysThrValAspIleTyrGlyHisValThrCysMetArgSer 120
QY 861 CAGAGAACTACATGTTGAGCGAGGACCAAGTACGTGTTTCATCATGAGCGGTGCTG 920
Db 121 GlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIleHisGluAlaLeuLeu 140
QY 921 GAGGCTGCCAGTGGCGGCACACAGAGTGGCTGCGCCCAACTGTATGCCACATCCAG 980
Db 141 GluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeuTyrAlaHisIleGln 160
QY 981 AAGCTGGGCAAGTGGCTCGAGGGAGAGTGGACCGCCATGAGCTGAGTTCAGTTG 1040

Db 161 LysLeuGlyGlnValProProGlyGluSerValThrAlaMetGluLeuGluPheLysLeu 180
QY 1041 CTGGCCAGCTCCAGGCCCACACGTCCTCCGCTTCATCAGCCCAACCTGCTGCAACAAG 1100
Db 181 LeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLys 200
QY 1101 TTCAGAACCGCTGCTGAAACATCATGCTAGCAATTGACCCGTGTGTCTCTGCAGCCC 1160
Db 201 PheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArgValCysLeuGlnPro 220
QY 1161 ATCCGTGTGTGGAGGCTCTGACTACATCAATGCCAGCTTCCTGGATGTTATAGACAG 1220
Db 221 IleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGln 240
QY 1221 CAGAAGGCTACATAGCTACACAGGGCTCTGACAGAGCCAGAGACCCAGGACTTCTGCGC 1280
Db 241 GlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThrGluAspPheTyrArg 260
QY 1281 ATGCTATGGAGACCAATTCCACCATCATGCTCATGCTGACCAAGCTTCGGGAGATGGC 1340
Db 261 MetLeuTyrGluHisAsnSerThrIleValMetLeuThrLysLeuArgGluMetGly 280
QY 1341 AGGAGAAATGCCACCACTACTGCGCAGCAGAGCGCTCTGCTCCCTACCACTACTTGT 1400
Db 281 ArgGluLysCysHisGlnTyrTyrProAlaGluArgSerAlaArgTyrGlnTyrPheVal 300
QY 1401 GTTGACCCGATGGCTGAGTACAACATGCCAGATATATCTCTGCTGAGTTCAAGTCAAG 1460
Db 301 ValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArgGluPheLysValThr 320
QY 1461 GATGCCCGGATGGGCACTCAAGACATCCGCGAGTTCAGTTCACAGCTGGCCAGAG 1520
Db 321 AspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPheThrAspTyrProGlu 340
QY 1521 CAGGCGCTGCCCAACAGACAGGCGGATTCATTGACTTCATCGGCGCAGGTGCATAAGACC 1580
Db 341 GlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGlyGlnValHisLysThr 360
QY 1581 AAGGAGCAAGTTGGACAGAGTGGGCTATCAGGTGCTGCTGCTGCTGCTGCTGCTGCTG 1640
Db 361 LysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSerAlaGlyValGlyArg 380
QY 1641 ACCGGGTGTTTCATCTCAGTCTGAGCATCTCTGAGCGCATGCTGAGGGGTGCTGCTG 1700
Db 381 ThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArgTyrGluGlyValVal 400
QY 1701 GACATGTTTCAGACCGTGAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1760
Db 401 AspMetPheGlnThrValLysThrLeuArgThrGlnArgProAlaMetValGlnThrGlu 420
QY 1761 GACCATATCAGTGTGTACCGTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1820
Db 421 AspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGlySerPheAspHisTyr 440
QY 1821 GCAACG 1826
Db 441 AlaThr 442

RESULT 4
US-10-374-539-3
Sequence 3, Application US/10374539
Publication No. US20030195247A1
GENERAL INFORMATION:
APPLICANT: SUNESIS PHARMACEUTICALS, INC.
APPLICANT: BARR, Kenneth
APPLICANT: FAHR, Bruce
APPLICANT: HANSEN, Stig
APPLICANT: McDOWELL, Robert
APPLICANT: WIESMAN, Chris
APPLICANT: ZHU, Jian
TITLE OF INVENTION: COMPOUNDS THAT MODULATE THE ACTIVITY OF
TITLE OF INVENTION: PTP-1B AND TC-PTP
FILE REFERENCE: 39750-0008

CURRENT APPLICATION NUMBER: US/10/374,539

CURRENT FILING DATE: 2003-02-25

PRIOR APPLICATION NUMBER: US 60/361,475

PRIOR FILING DATE: 2002-03-01

NUMBER OF SEQ ID NOS: 29

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 296

TYPE: PRT

ORGANISM: Homo sapiens

US-10-374-539-3

Alignment Scores:

red. No.:	5,23e-260	Length:	296
Score:	296.00	Matches:	296
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	26.01%	Indels:	0
DB:	14	Gaps:	0

US-09-719-272-1 (1-3467) x US-10-374-539-3 (1-296)

102	CCCATCCAGCACTGGCGGACAAATCGAGCGCTCAAGCCAAAGCAACGATGGCTCAAGTTC	161
1	ProileThrAspLeuAlaAspAsnIleGluArgLeuAlaAsnAspGlyLeuLysPhe	20
162	TCCAGAGATCAGTCCATCGACCTGGACAGCAGTTCAGTGGGAGAAATCAAACTG	221
21	SerGlnGluTrpGluSerIleAspProGlyGlnPheThrTrpGluAsnSerAsnLeu	40
222	GAGTGAACCAAGCCCAAGAACCCCTATGCAATGTCATCGCTACGACCACTTCGAGTC	281
41	GluValAsnLysProLysAsnArgTrpAlaAsnValIleAlaTrpAspHisSerArgVal	60
282	ATCTTACCTCTATCATGCGTCCCGGAGTGAATGACTACATCAATGCCAATCATCGAT	341
61	IleLeuThrSerIleAspGlyValProGlySerAspTrpIleAsnAlaAsnTrpIleAsp	80
342	GGTACCGCAAGCAGAAATGCTCATCGCTACGCGAGCGCCCTGCGGAGCAATGGGC	401
81	GlyTyArgLysGlnAsnAlaTrpIleAlaThrGlnGlyProLeuProGluThrMetGly	100
402	GATTCTGGAGATGGTGGGACAGCGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	461
101	AspPheTrpArgMetValTrpGluGlnArgThrAlaThrValValMetThrArgLeu	120
462	GAGGAGAAAGTCCCGGTAAATGTGATCAGTACGCGAGCGCCCTGCGGAGCAATGGGC	521
121	GluGluLysSerArgValLysCysAspGlnTrpProAlaArgGlyThrGluThrCys	140
522	GGCCTTATTCAGTGACCTGTGGACACAGTGGAGCTGGCCACATACACTGGCGCAC	581
141	GlyLeuIleGlnValThrLeuLeuAspThrValGluLeuAlaThrTrpValArgThr	160
582	TTGCACTCCACAGAGTGGCTCCAGTGAAGCGTGAAGTGGTCAATGCTCAATGCTCATG	641
161	PheAlaLeuHisLysSerGlySerGlyArgGluLeuArgGlnPheGlnPheMet	180
642	GCCTGGCCAGACCATGGAGTTCCTGAGTACCCCACTCCCTGCTGCTGCTGCTGCTGCTG	701
181	AlaTrpProAspHisGlyValProGluTrpProThrProIleLeuAlaPheLeuArg	200
702	GTCAAGCCTTCAACCCCTAGACGAGGAGCCCATGGTGGTGCATCGCGCGGCGGTG	761
201	ValLysAlaCysAsnProLeuAspAlaGlyProMetValIleHisCysSerAlaGlyVal	220
762	GGCGCACCGGCTCTTCATGCTGATGTGCCATGTGTGGAGCGGATGAAGCACGAGAAG	821
221	GlyArgThrGlyCysPheIleValIleAspAlaMetLeuGluArgMetLysHisGluLys	240
822	ACGCTGACATCTATGGCCAGCTGACCTGCATCGCATCACAGAGCACTACATGGTGCAG	881
241	ThrValAspIleTrpGlyHisValThrCysMetArgSerGlnArgAsnTrpMetValGln	260

Qy	882	ACGAGAGACAGTACGTGTTTCATCCATGAGCGCTGAGAGCTCCAGCTGCGGCAC	941
Db	261	ThrGluAspGlnTrpValPheIleHisGluAlaLeuLeuAlaThrCysGlyHis	280
Qy	942	ACAGAGTGCCTGCCCGCAACCTGTATGCCACATCCAGAGCTGGGC	989
Db	281	ThrGluValProAlaArgAsnLeuTrpAlaHisIleGlnLysLeuGly	296

RESULT 5

US-10-374-499-9
; Sequence 9, Application US/10374499
; Publication No. US20040005632A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: ERLANSON, Daniel A.
; APPLICANT: MCDOWELL, Robert S.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING COMPOUNDS THAT
; TITLE OF INVENTION: MODULATE ENZYMACTIC ACTIVITY
; FILE REFERENCE: 39750-0016
; CURRENT APPLICATION NUMBER: US/10/374,499
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/377,034
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US 10/121,216
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-499-9

Alignment Scores:

Pred. No.:	5,23e-260	Length:	296
Score:	296.00	Matches:	296
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	26.01%	Indels:	0
DB:	15	Gaps:	0

US-09-719-272-1 (1-3467) x US-10-374-499-9 (1-296)

Qy	102	CCCATCCAGCACTGGCGGACAAATCGAGCGCTCAAGCCAAAGCAACGATGGCTCAAGTTC	161
Db	1	ProileThrAspLeuAlaAspAsnIleGluArgLeuAlaAsnAspGlyLeuLysPhe	20
Qy	162	TCCAGAGATCAGTCCATCGACCTGGACAGCAGTTCAGTGGGAGAAATCAAACTG	221
Db	21	SerGlnGluTrpGluSerIleAspProGlyGlnPheThrTrpGluAsnSerAsnLeu	40
Qy	222	GAGTGAACCAAGCCCAAGAACCCCTATGCAATGTCATCGCTACGACCACTTCGAGTC	281
Db	41	GluValAsnLysProLysAsnArgTrpAlaAsnValIleAlaTrpAspHisSerArgVal	60
Qy	282	ATCTTACCTCTATCATGCGTCCCGGAGTGAATGACTACATCAATGCCAATCATCGAT	341
Db	61	IleLeuThrSerIleAspGlyValProGlySerAspTrpIleAsnAlaAsnTrpIleAsp	80
Qy	342	GGTACCGCAAGCAGAAATGCTCATCGCTACGCGAGCGCCCTGCGGAGCAATGGGC	401
Db	81	GlyTyArgLysGlnAsnAlaTrpIleAlaThrGlnGlyProLeuProGluThrMetGly	100
Qy	402	GATTCTGGAGATGGTGGGACAGCGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	461
Db	101	AspPheTrpArgMetValTrpGluGlnArgThrAlaThrValValMetThrArgLeu	120
Qy	462	GAGGAGAAAGTCCCGGTAAATGTGATCAGTACGCGAGCGCCCTGCGGAGCAATGGGC	521
Db	121	GluGluLysSerArgValLysCysAspGlnTrpProAlaArgGlyThrGluThrCys	140
Qy	522	GGCCTTATTCAGTGACCTGTGGACACAGTGGAGCTGGCCACATACACTGGCGCAC	581

Db 141 GlyLeuIleGlnValThrLeuLeuAspThrValGluLeuAlaThrThrValArgThr 160
2y 582 TTGCGACTCCACAGAGTGGCTCAGTGAAGACCGTGGCTGCTCAGTTTCAGTTTCATG 641
Db 161 PheAlaLeuHisLysSerGlySerGluLysArgGluLeuArgGlnPheGlnPheMet 180
2y 642 GCTGGCCAGACCATGAGTTCCTGAGTACCCCACTCCCATCTGCGCTTCTTACGACGG 701
Db 181 AlaTrpProAspHisGlyValProGluLysProThrProLeuAlaPheLeuArgArg 200
2y 702 GTCAAGCCCTGCAACCCCTAGACGCGAGGCCCATCGTGTGTGTCACATGCGAGCGGCGTG 761
Db 201 ValLysAlaCysAsnProLeuAspAlaGlyProMetValHisCysSerAlaGlyVal 220
2y 762 GCGCGCACCGCTGCTTCATCGTATTGATGATGATGATGATGATGATGATGATGATGAT 821
Db 221 GlyArgThrGlyCysPheIleValIleAspAlaMetLeuGluArgMetLysHisGluLys 240
2y 822 ACGGTGACATCTATGCGCACGCTGACCTGATCGATCGATCGATCGATCGATCGATCGAT 881
Db 241 ThrValAspIleThrGlyHisValThrCysMetArgSerGlnArgAsnThrMetValGln 260
2y 882 ACGGAGACAGTACGCTTCATCCATGAGCGCTGCTGAGGCTGCGACGTGCGGCCAC 941
Db 261 ThrGluAspGlnThrValPheIleHisGluAlaLeuLeuGluAlaAlaThrCysGlyHis 280
2y 942 ACAGAGTGGCTGCGCCGCAACCTGTATGTCCTCCCATCCAGAGTGGGC 989
Db 281 ThrGluValProAlaArgAsnLeuThrAlaHisIleGlnLysLeuGly 296

RESULT 6

US-10-314-232-13
; Sequence 13, Application US/10314232
; Publication No. US20030138932A1
; GENERAL INFORMATION:
; APPLICANT: MOLLER, NIELS P.H.
; APPLICANT: MOLLER, KARIN B.
; APPLICANT: ULLRICH, AXEL
; TITLE OF INVENTION: PTP-331: A NOVEL PROTEIN TYROSINE PHOSPHATASE
; FILE REFERENCE: 038602/0886
; CURRENT APPLICATION NUMBER: US/10/314,232
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/361,096
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 08/449,609
; PRIOR FILING DATE: 1995-05-24
; PRIOR APPLICATION NUMBER: 08/036,210
; PRIOR FILING DATE: 1995-03-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LAR
US-10-314-232-13

Alignment Scores:

Pred. No.:	1,23e-253	Length:	289
Score:	289.00	Matches:	289
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	25.40%	Indels:	0
DB:	14	Gaps:	0

US-09-719-272-1 (1-3467) x US-10-314-232-13 (1-289)

Qy 81 ATGCGAGACCCACCCATCCCATCCAGTCCGCGGAGCAACATCGAGCGCTCAA 140
Db 1 MetArgAspHisProPheIleProIleThrAspLeuAlaAspAsnIleGluArgLeuLys 20

Qy 141 GCCAACGATGGCTCAAGTTCTCCAGGAGTATGAGTCCATCCAGCCCTGGACAGCATTC 200
Db 21 AlaAsnAspGlyLeuLysPheSerGlnLysThrGluSerIleAspProGlyGlnGlnPhe 40
Qy 201 ACGTGGGAGAAATTCAAACCTGGAGGTGAACAAGCCCAAGAACCGCTATGGAATGTCATC 260
Db 41 ThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArgTrpAlaAsnValIle 60
Qy 261 GCCTACGACCACTCTCGAGTCATCTTACCTCTATCGATGGCTGCCGGGAGTGTACTAC 320
Db 61 AlaTrpAspHisSerArgValIleLeuThrSerIleAspGlyValProGlySerAspTrp 80
Qy 321 ATCAATGCCAATCATCATGCTGCTACCGCAAGCAGAAATGCCTACATCGCCACGCGAGGC 380
Db 81 IleAsnAlaAsnTrpIleAspGlyTrpArgLysGlnAsnAlaTrpIleAlaThrGlnGly 100
Qy 381 CCCGTGCCGACGACCATCGGCGCATTTCTGGAGAATGTTGGGAACAGCGCACGGCACT 440
Db 101 ProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGluGlnArgThrAlaThr 120
Qy 441 GTGTCATGATGACACCGCTGGAGGAGAGTCCCGGTAAATGTGATCAGTACTGTGCCCA 500
Db 121 ValValMetMetThrArgLeuGluLysSerArgValLysCysAspGlnTrpPro 140
Qy 501 GCCGTGGCACCCGAGACCTGTGGCCTTATTACAGGTGACCTGTGGACACAGTGGAGCTG 560
Db 141 AlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeuAspThrValGluLeu 160
Qy 561 GCCACATACATGTGGCGACCTTCGCTGCTCCACAGAGTGGCTCCAGTGAAGCGTGAG 620
Db 161 AlaThrTrpValArgThrPheAlaLeuHisLysSerGlySerGluLysArgGlu 180
Qy 621 CTGGCTCAGTTTTCAGTTTCATGGCTGCGCACACCATGAGTTCCTGAGTACCCCAACTCCC 680
Db 181 LeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGluTrpPro 200
Qy 681 ATCTGTGGCTTCTTACGAGCGGTCAAGCGCTGCAACCCCTAGACGCGAGGCCCATCGTG 740
Db 201 IleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAspAlaGlyProMetVal 220
Qy 741 GTGCACTGACGCGGGCGTGGCGCGCACCGCTGCTTCATCGTGTGATTCATCGCTGTG 800
Db 221 ValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeu 240
Qy 801 GAGCGGATGAAGCAGCAGAGAACGCGTGACATCTATGCGCACGCTGACCTGATCGATCA 860
Db 241 GluArgMetLysHisGluLysThrValAspIleThrValAspIleThrCysMetArgSer 260
Qy 861 CAGAGGAATCATGCTGCTGACGAGGACGAGTACGTTTCATCCATGAGCGCTGCTG 920
Db 261 GlnArgAsnTrpMetValGlnThrGluAspGlnTrpValPheIleHisGluAlaLeu 280
Qy 921 GAGGCTGCCACGTCGCGCCACACAGAG 947
Db 281 GluAlaAlaThrCysGlyHisThrGlu 289

RESULT 7

US-09-788-626-8
; Sequence 8, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 306
; TYPE: PRT

ORGANISM: *Homo sapiens*

JS-09-788-626-8

Alignment Scores:

Length:	1.73e-174	306
Matches:	202.00	250
Conservative:	97.66%	0
Mismatches:	97.66%	0
Indels:	17.75%	6
Gaps:	9	0

US-09-719-272-1 (1-3467) x US-09-788-626-8 (1-306)

[illegible]

RESULT 8

US-09-788-626-27

; Sequence 27, Application US/09788626

Patent No. US20020009762A1

GENERAL INFORMATION:

APPLICANT: Flint, Andrew J.

APPLICANT: Cool, Deborah E.

TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE

```

; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788.626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-788-626-27

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Alignment scores:

Pred. No.:	6.15e-170	Length:	294
Score:	197.00	Matches:	245
Percent Similarity:	97.61%	Conservative:	0
Best Local Similarity:	97.61%	Mismatches:	6
Query Match:	17.31%	Indels:	0
DB:	9	Gaps:	0

US-09-719-272-1 (1-3467) x US-09-788-626-27 (1-294)

1062	QY	ACGTCCCGCTTCATCAGCGCCAACTCGCCCTGCAACAAGTTCAAGACCGCGTGTGTGAC	1121
1	Db	1 ThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsnArgLeuValAsn	20
1122	QY	ATCATGCGCTCAGAAATGACCGGTGTGTGCTGACGCCCATCCGTGGTGTGAGGGCTCT	1181
21	Db	11leMetProTyrgluLeuThrArgValCysLeuGlnProIleArgGlyValGluGlySer	40
1182	QY	GACTACATCAATGCCAGCTTCCTGGATGGTTATAGACAGCAGAGCGCTCATAGCTACA	1241
41	Db	41AspTyrlleAsnAlaSerPheLeuAspGlyTyArgGlnGlnLysAlaTyrlleAlaThr	60
1242	QY	CAGGGCGCTCTGCGCAGAGACACCAGGACTCTCTGGCGCATCTGCTATGGCAGACACAATCC	1301
61	Db	61GlnGlyProLeuAlaGlnSerThrGluAspPheTrpArgMetLeuTrpGluHisAsnSer	80
1302	QY	ACCATCATCGTCATGCTGACCAAGCTTCGGGAGATGGCAGGAGAGAAATGCCACCAGTAC	1361
81	Db	81ThrIleIleValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTy	100
1362	QY	TGGCCACGACAGCGCTCTCGCTACCACTACTTTGTTGTCACCCGATGGCTGAGTAC	1421
101	Db	101TrpProAlaGluArgSerAlaArgTyrglnTyPheValValAspProMetAlaGlnTy	120
1422	QY	AACATGCCCGCATATATCTCGGTGAGTTCAAGTTCACGATGCCGGATGGCGAGTCA	1481
121	Db	121AsnMetProGlnTyrlleLeu-----PheLysValThrAspAlaArgAspGlyGlnSer	138
1482	QY	AGGACAACTCCGCGAGTTCCAGTTCAAGACTCGCCAGACAGCGCGCTGCCCAAGACAGGC	1541
139	Db	139ArgThrIleArgGlnPheGlnPheThrAspTrpProGluGlnGlyValProLysThrGly	158
1542	QY	GAGGGATTCATTGATTCATCGGCGAGTGTGCATAGACCAAGCAGCAGTTCGACAGGAT	1601
159	Db	159GluGlyPheIleAspPheIleGlyGlnValHisLysThrLysGluGlnPheGlyGlnAsp	178
1602	QY	GGCGCTTATCAGCGTGACGTCAGTGTGCGTGGCGGCCGACCGGGGTGTTCATCACTCG	1661
179	Db	179GlyProIleThrValHisCysSerAlaGlyValGlyArgThrGlyValPheIleThrLeu	198
1662	QY	AGCATCGTCTGAGGGCGATCGCCTATGAGCGGTGGTGCATGTTTCAGACCGGTGAAG	1721
199	Db	199SerIleValLeuGluArgMetArgTyrgluGlyValValAspMetPheGlnThrValLys	218
1722	QY	ACCTCGGTACACAGCGTCTCGCATGTGTGCACAGAGACCAAGTATCAGCTGTGCTAC	1781
219	Db	219ThrIleuArgThrGlnArgProAlaMetValGlnThrGluAspGlnTyrglnLeuCysTy	238
1782	QY	CGTCCGCGCCCTGAGTACCTTC	1802
239	Db	ArgAlaAlaLeuGluTyrlleu	245

RESULT 9

US-09-808-602-54

; Sequence 54, Application US/09808602

; Patent No. US20020155115A1

; GENERAL INFORMATION:

; APPLICANT: Vernet, Corine A

; APPLICANT: Fernandes, Elma

; APPLICANT: Shimkets, Richard A

; APPLICANT: Herrmann, John L

; APPLICANT: Majumder, Kumud

; APPLICANT: Mishra, Vishnu

; APPLICANT: Mezes, Peter S

; APPLICANT: MacDougall, John

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 15966-697 CIP

; CURRENT APPLICATION NUMBER: US/09/808,602

; PRIOR FILING DATE: 2001-03-14

; PRIOR APPLICATION NUMBER: 09/800,198

; PRIOR FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: 60/186,596

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 54

; LENGTH: 1502

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-808-602-54

Alignment Scores:

Pred. No.:	1.75e-44	Length:	1502
Score:	59.00	Matches:	59
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.18%	Indels:	0
DB:	9	Gaps:	0

US-09-719-272-1 (1-3467) x US-09-808-602-54 (1-1502)

QY	1311	GTCTGCTGACCAAGCTTCGGGAGATGGCGAGGAGAAATGCCACCACTACTGGCCAGCA	1370
DB	1331	ValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyTrpProAla	1350
QY	1371	GAGCGCTCTGCTCGCTACAGTACTTTGTTGACCGATGGCTGAGTACAAATGCC	1430
DB	1351	GluArgSerAlaArgTyGlnTyPheValValAspProMetAlaGluTyAsnMetPro	1370
QY	1431	CAGTATATCTCGTGGAGTTCAGGTCAAGTCCCGGATGGCGAGTCAAGGACA	1487
DB	1371	GlnTyTrpLeuArgGluPheLysValThrAspAlaArgAspGlyGlnSerArgThr	1389

RESULT 10

US-09-800-198-44

; Sequence 44, Application US/09800198

; Publication No. US20030087816A1

; GENERAL INFORMATION:

; APPLICANT: Vernet, Corine A

; APPLICANT: Fernandes, Elma

; APPLICANT: Shimkets, Richard A

; APPLICANT: Herrmann, John L

; APPLICANT: Majumder, Kumud

; APPLICANT: Mishra, Vishnu

; APPLICANT: Mezes, Peter S

; APPLICANT: Rastelli, Luca

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 15966-697

; CURRENT APPLICATION NUMBER: US/09/800,198

; PRIOR FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: 60/186,596

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 98

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 44

; LENGTH: 1502

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-800-198-44

Alignment Scores:

Pred. No.:	1.75e-44	Length:	1502
Score:	59.00	Matches:	59
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.18%	Indels:	0
DB:	10	Gaps:	0

US-09-719-272-1 (1-3467) x US-09-800-198-44 (1-1502)

QY	1311	GTCTGCTGACCAAGCTTCGGGAGATGGCGAGGAGAAATGCCACCACTACTGGCCAGCA	1370
DB	1331	ValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyTrpProAla	1350
QY	1371	GAGCGCTCTGCTCGCTACAGTACTTTGTTGACCGATGGCTGAGTACAAATGCC	1430
DB	1351	GluArgSerAlaArgTyGlnTyPheValValAspProMetAlaGluTyAsnMetPro	1370
QY	1431	CAGTATATCTCGTGGAGTTCAGGTCAAGTCCCGGATGGCGAGTCAAGGACA	1487
DB	1371	GlnTyTrpLeuArgGluPheLysValThrAspAlaArgAspGlyGlnSerArgThr	1389

RESULT 11

US-09-808-602-55

; Sequence 55, Application US/09808602

; Patent No. US20020155115A1

; GENERAL INFORMATION:

; APPLICANT: Vernet, Corine A

; APPLICANT: Fernandes, Elma

; APPLICANT: Shimkets, Richard A

; APPLICANT: Herrmann, John L

; APPLICANT: Majumder, Kumud

; APPLICANT: Mishra, Vishnu

; APPLICANT: Mezes, Peter S

; APPLICANT: MacDougall, John

; TITLE OF INVENTION: NO. US20020155115A1el Proteins and Nuclec Acids Encoding Same

; FILE REFERENCE: 15966-697 CIP

; CURRENT APPLICATION NUMBER: US/09/808,602

; CURRENT FILING DATE: 2001-03-14

; PRIOR APPLICATION NUMBER: 09/800,198

; PRIOR FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: 60/186,596

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 55

; LENGTH: 1948

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-808-602-55

Alignment Scores:

Pred. No.:	1.69e-44	Length:	1948
Score:	59.00	Matches:	59
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.18%	Indels:	0
DB:	9	Gaps:	0

US-09-719-272-1 (1-3467) x US-09-808-602-55 (1-1948)

QY	1311	GTCTGCTGACCAAGCTTCGGGAGATGGCGAGGAGAAATGCCACCACTACTGGCCAGCA	1370
DB	1377	ValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyTrpProAla	1796
QY	1371	GAGCGCTCTGCTCGCTACAGTACTTTGTTGACCGATGGCTGAGTACAAATGCC	1430

db 1797 GluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetPro 1816
1431 CAGTATATCTCGTGGAGTTCAGAGTCAAGATGCCCGGATGGCGGATCAAGGACA 1487
1817 GlnTyrIleLeuArgGluPheValThrAspAlaArgAspGlyGlnSerArgThr 1835
RESULT 12
JS-09-800-198-45
Sequence 45, Application US/09800198
Publication No. US20030087816A1
GENERAL INFORMATION:
APPLICANT: Vernet, Cornie AM
APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard A
APPLICANT: Herrmann, John L
APPLICANT: Majumder, Kumud
APPLICANT: Mishra, Vishna
APPLICANT: Mezes, Peter S
APPLICANT: Rastelli, Luca
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-697
CURRENT APPLICATION NUMBER: US/09/800,198
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 45
LENGTH: 1948
TYPE: PRT
ORGANISM: Homo sapiens
JS-09-800-198-45
Alignment Scores:
Pred. No.: 1.69e-44 Length: 1948
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
DB: 10 Gaps: 0
JS-09-719-272-1 (1-3467) x US-09-800-198-45 (1-1948)
2y 1311 GTCATGCTGACCAAGCTTCGGAGATGGCAGGAGAAATGCCACAGTACTGGCCAGCA 1370
db 1777 ValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAla 1796
2y 1371 GAGCGCTCTGCTCGCTACCAAGTACTTTGTTGACCCGATGGCTGAGTACACATGCC 1430
db 1797 GluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetPro 1816
2y 1431 CAGTATATCTCGTGGAGTTCAGAGTCAAGATGCCCGGATGGCGGATCAAGGACA 1487
db 1817 GlnTyrIleLeuArgGluPheValThrAspAlaArgAspGlyGlnSerArgThr 1835
RESULT 13
JS-10-029-386-29636
Sequence 29636, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AECMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 29636
LENGTH: 57
TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC011772.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.95
OTHER INFORMATION: SWISSPROT HIT: O00470, EVALUE 1.20e+00
US-10-029-386-29636
Alignment Scores:
Pred. No.: 1.2e-40 Length: 57
Score: 55.00 Matches: 55
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.86% Indels: 0
DB: 14 Gaps: 0
US-09-719-272-1 (1-3467) x US-10-029-386-29636 (1-57)
Qy 476 CCGGACTTCCTCCAGCCGTGTCTCATCATGACACACAGTGGCGCTGCTTCCACAC 417
Db 3 ProGlyLeuLeuLeuGlnProCysHisHisAspHisSerGlyArgAlaLeuPheProHis 22
Qy 416 CATTCTCCAGAAATCGCCCATGGTCTCGGACAGGGGCCCTGGTGGCGATGAGGCATT 357
Db 23 HisSerProGluIleAlaHisGlyLeuGlyGlnGlyAlaLeuArgGlyAspValGlyIle 42
Qy 356 CTGCTTGGGTAGCATCGATGATGTTGGCATTGATGATGATGATGATGATGATGATGAT 312
Db 43 LeuLeuAlaValAlaIleAspValValGlyIleAspValValThr 57
RESULT 14
US-10-258-666-12
Sequence 12, Application US/10258666
Publication No. US20040005578A1
GENERAL INFORMATION:
APPLICANT: Yamada, Yoji
APPLICANT: Sekine, Susumu
APPLICANT: Kikuchi, Yasuhiro
APPLICANT: Sakurada, Kazuhiro
APPLICANT: Kyowa Hakko Kogyo Co., Ltd.
TITLE OF INVENTION: Myocardial Cell Proliferation-Associated Genes
FILE REFERENCE: 082382-000000US
CURRENT APPLICATION NUMBER: US/10/258,666
CURRENT FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: JP 2000-126741
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: WO PCT/JP01/03700
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 1495
TYPE: PRT
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: RHDH-231, PTP-PI
US-10-258-666-12
Alignment Scores:
Pred. No.: 3.39e-27 Length: 1495
Score: 40.00 Matches: 40
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.51% Indels: 0
DB: 15 Gaps: 0
US-09-719-272-1 (1-3467) x US-10-258-666-12 (1-1495)

Search completed: March 9, 2004, 09:17:35
Job time : 149 secs

GenCore version 5.1.6
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DN nucleic - protein search, using frame_plus_n2p model
Run on: March 9, 2004, 08:52:58 ; Search time 34.5 Seconds
(without alignments)
10465.347 Million cell updates/sec

Title: US-09-719-272-1
Perfect score: 1138
Sequence: 1 gatccgactgaaggactcc.....atttgataatcagattttc 3467

Scoring table:
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Xgapop 60.0, Xgapext 60.0
Ygapop 60.0, Ygapext 60.0
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

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Word size: 1

Total number of hits satisfying chosen parameters: 283186

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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-DB=SwissProt_42 -OPWT=fastan -SUFFIX=rsrp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09719272 @CGN 1.1.37 @runat_09032004.085229.7437 -NCPU=6 -ICPU=3
-NO MWAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPOPEXT=60 -FGAPOP=6
-FGAPOPEXT=7 -YGAPOP=60 -YGAPOPEXT=60 -DELOP=6 -DELOPEXT=7

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	607	53.3	1897	1 PTPF HUMAN	P10586 homo sapien
2	59	5.2	1912	1 PTPD HUMAN	P23468 homo sapien
3	59	5.2	1948	1 PTNS HUMAN	Q13332 homo sapien
4	34	3.0	2029	1 LAR DROME	P16621 drosophila
5	22	1.9	114	1 PT13 STYPL	P28205 styela plic
6	22	1.1	521	1 PTF1 DICDI	P34137 dictyosteli
7	12	1.1	699	1 PTFE MOUSE	P49446 mus musculus
8	12	1.1	700	1 PTFE HUMAN	P23469 homo sapien
9	12	1.1	796	1 PTRA RAT	Q03348 rattus norv
10	12	1.1	802	1 PTRA HUMAN	P18433 homo sapien
11	12	1.1	829	1 PTRA MOUSE	P18052 mus musculus
12	12	1.1	1152	1 CD45 MOUSE	P06800 mus musculus
13	12	1.1	1174	1 PTNL HUMAN	Q16825 homo sapien
14	12	1.1	1175	1 PTNL RAT	Q62728 rattus norv
15	12	1.1	1176	1 PTNL MOUSE	Q62136 mus musculus
16	12	1.1	1187	1 PTNE HUMAN	Q15678 homo sapien
17	12	1.1	1189	1 PTNE MOUSE	Q62130 mus musculus
18	12	1.1	1255	1 CD45 RAT	P04157 rattus norv

19	12	1.1	1301	1 PTP9 DROME	P35832 drosophila
20	12	1.1	1304	1 CD45 HUMAN	P08575 homo sapien
21	12	1.1	1422	1 PTPG CHICK	Q98936 gallus gall
22	12	1.1	1439	1 PTPK HUMAN	Q15262 homo sapien
23	12	1.1	1454	1 PTPT MOUSE	Q99m80 mus musculu
24	12	1.1	1463	1 PTPT HUMAN	Q14522 homo sapien
25	12	1.1	1497	1 PTPB HUMAN	P23467 homo sapien
26	12	1.1	2314	1 PTPZ HUMAN	P23471 homo sapien
27	12	1.1	2316	1 PTPZ RAT	Q62656 rattus norv
28	11	1.0	335	1 PTP1 YEAST	P25044 saccharomyc
29	11	1.0	550	1 PTP1 SCHRO	P27574 schizosacch
30	11	1.0	595	1 PTN6 HUMAN	P29350 homo sapien
31	11	1.0	711	1 PYP2 SCHRO	P32586 schizosacch
32	11	1.0	1216	1 PTP0 HUMAN	Q16827 homo sapien
33	11	1.0	1238	1 PTPJ MOUSE	Q64455 mus musculu
34	11	1.0	1337	1 PTPJ HUMAN	Q12913 homo sapien
35	11	1.0	1430	1 PTPU HUMAN	Q92729 homo sapien
36	11	1.0	1442	1 PTPG MOUSE	Q05909 mus musculu
37	11	1.0	1445	1 PTPG HUMAN	P23470 homo sapien
38	11	1.0	1462	1 PTP6 DROME	P16620 drosophila
39	11	1.0	1705	1 PTFV MOUSE	P70289 mus musculu
40	11	1.0	1711	1 PTFV RAT	Q64612 rattus norv
41	11	1.0	2200	1 LAR CAEL	Q96mn8 caenorhabdi
42	10	0.9	303	1 PYP3 SCHRO	P32587 schizosacch
43	10	0.9	458	1 PTNI HUMAN	Q99552 homo sapien
44	10	0.9	595	1 PTN6 MOUSE	P29351 mus musculu
45	10	0.9	613	1 PTN6 RAT	P81718 rattus norv

ALIGNMENTS

RESULT 1
PTPF_HUMAN STANDARD; PRT; 1997 AA.
AC P10586;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE LAR protein precursor (Leukocyte antigen related) (EC 3.1.3.48).
GN PTPRF OR LAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tonsil;
RX MEDLINE=89035978; PubMed=2972792;
RA Streuli M., Krueger N.X., Hall L.R., Schlossman S.F., Saito H.;
RT "A new member of the immunoglobulin superfamily that has a
RT cytoplasmic region homologous to the leukocyte common antigen."
RL J. Exp. Med. 168:1523-1530(1988).
RN [2]
RP MUTAGENESIS.
RX MEDLINE=90046860; PubMed=2554325;
RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;
RT "A family of receptor-linked protein tyrosine phosphatases in humans
RT and Drosophila."
RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).
RN [3]
RP MUTAGENESIS.
RX MEDLINE=90316093; PubMed=1695146;
RA Streuli M., Krueger N.X., Tsai T., Tang M., Saito H.;
RT "Distinct functional roles of the two intracellular phosphatase like
RT domains of the receptor-linked protein tyrosine phosphatases LCA and
RT LAR."
RL EMBO J. 9:2399-2407(1990).
CC -|- FUNCTION: It is possible that DLAR is a cell adhesion receptor.
CC It possesses an intrinsic protein tyrosine phosphatase activity
CC (PTPase).
CC -|- FUNCTION: The first PTPase domain has enzymatic activity, while
CC the second one seems to affect the substrate specificity of the
CC first one.


```
b 1631 LeuGluPheLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 1650
y 1086 CTGCGCTGCAACAAGTTCAAGAACCGCTGTTGAACATCATCCCTACGAATTCACCGT 1145
b 1651 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 1670
y 1146 CTGTGCTCAGCCCATCGTGGTGGAGGCTGTGACTACATCAATGCCAGCTTCCTG 1205
b 1671 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu 1690
y 1206 GATGTTATAGACAGCAGAGCCCTACATAGCTACACAGGGCCCTCTGCAGAGACACC 1265
b 1691 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr 1710
y 1266 GAGGACTTCGGCGCATGTATGGGAGCAATTCACCATCATGTCATGCTGACCAAG 1325
b 1711 GluAspPheTyrArgMetLeuTyrGluHisAsnSerThrIleValMetLeuThrLys 1730
y 1326 CTTCGGGAGATGGCAGGAGAAATGCCACCACTACTGCCACAGCAGCGCTCTCTCGC 1385
b 1731 LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 1750
y 1386 TACAGTACTTTGTTGACCGCATGGCTGAGTACATCAATGCCCGCATATATCTGGT 1445
b 1751 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 1770
y 1446 GAGTTCAGGTCAAGTACCGGATGCCGGATGGCAGTCAAGACAAATCCGAGTTCAGTTC 1505
b 1771 GluPheLysValThrAspAlaArgGlyGlnSerArgThrIleArgGlnPheGlnPhe 1790
y 1506 ACAGACTGCGCAGCAGCGCGTGCACAGAGCGAGGAGTATCATCTCATCTCGCG 1565
b 1791 ThrAspTrpProGlnGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 1810
y 1566 CAGTCAATAGACAGGAGCGATTTGACAGGATGGCCATCATCGTGCAGTGCAGT 1625
b 1811 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1830
y 1626 GCTGGGTGGCGCGCACCGGGGTTCATCATCTCTGAGCATCTCTGAGCGCATGCGC 1685
b 1831 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 1850
y 1686 TATGAGGCGTGTGTCATGTTTCAGACCGTGAAGCCTGGTACACAGGCTCGCTCGC 1745
b 1851 TyrGluGlyValValAspMetPheGlnThrValIleThrLeuArgThrGlnArgProAla 1870
y 1746 ATGCTGACAGACAGGACCACTATCATCTGTGCTACCGTGGCGCCCTGGAGTACCTCGC 1805
b 1871 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly 1890
y 1806 AGCTTGACCACTATGCAAG 1826
b 1891 SerPheAspHisTyrAlaThr 1897

RESULT 2
ID -PTPD HUMAN STANDARD; PRT; 1912 AA.
AC P23468;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-
DE delta).
EN PTPRD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.
RX MEDLINE=95204468; PubMed=7896816;
RA Pulido R., Krueger N.X., Serria-Pages C., Saito H., Streuli M.,
```

```
RT "Molecular characterization of the human transmembrane protein-
RT tyrosine phosphatase delta. Evidence for tissue-specific expression of
RT alternative human transmembrane protein-tyrosine phosphatase delta
RT isoforms.";
RT J. Biol. Chem. 270:6722-6728 (1995).
RP [2]
RP SEQUENCE OF 390-1912 FROM N.A.
RC TISSUE=Placenta;
RC MEDLINE=91006018; PubMed=2170109;
RA Krueger N.X., Streuli M., Saito H.;
RT "Structural diversity and evolution of human receptor-like protein
RT tyrosine phosphatases.";
RL EMBL J. 9:3241-3252 (1990).
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=P23468-1; Sequence=Displayed;
CC Name=2; Synonyms=Kidney;
CC IsoId=P23468-2; Sequence=VSP_005147, VSP_005148, VSP_005149;
CC Name=3; Synonyms=Retal brain;
CC IsoId=P23468-3; Sequence=VSP_005150;
CC -1- PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
CC FROM THE TRANSMEMBRANE SEGMENT.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 8 fibronectin type III domains.
CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; L38929; AAC41749.1; -.
CC EMBL; X54133; CAA38068.1; -.
CC PIR; A56178; A56178.
CC HSSP; P18052; 1YFO.
CC Genew; HGNC:9668; PTPRD.
CC MIM; 601598; -.
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0005001; P: transmembrane receptor protein tyrosine pho. . . ; TAS.
CC GO; GO:0006470; P: protein amino acid dephosphorylation; TAS.
CC GO; GO:0007185; P: transmembrane receptor protein tyrosine pho. . . ; TAS.
CC InterPro; IPR008957; FN III-like.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR003962; FN III subd.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_C2.
CC InterPro; IPR000387; Tyr_phosphatase.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00041; fn3; 8.
CC Pfam; PF00047; ig; 3.
CC Pfam; PF0102; Y_phosphatase; 2.
CC PRINTS; PR00014; ENTYPRII.
CC PRINTS; PR00700; PRTYPHPTASE.
CC SMART; SM00060; FN3; 8.
CC SMART; SM00408; IGC2; 2.
CC SMART; SM00194; PTPC; 2.
CC PROSITE; PS00835; IG LIKE; 3.
CC PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
CC PROSITE; PS00566; TYR_PHOSPHATASE 2; 2.
CC PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase; Receptor; Glycoprotein; signal; Transmembrane; Repeat;
KW Immunoglobulin domain; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 1912
FT DOMAIN 21 1265
FT PROTEIN-TYROSINE PHOSPHATASE DELTA.
FT EXTRACELLULAR (POTENTIAL).
```

"Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta. Evidence for tissue-specific expression of alternative human transmembrane protein-tyrosine phosphatase delta isoforms.";

J. Biol. Chem. 270:6722-6728 (1995).

[2]

SEQUENCE OF 390-1912 FROM N.A.

TISSUE=Placenta;

MEDLINE=91006018; PubMed=2170109;

Krueger N.X., Streuli M., Saito H.;

"Structural diversity and evolution of human receptor-like protein

tyrosine phosphatases.";

EMBL J. 9:3241-3252 (1990).

-1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein

tyrosine + phosphate.

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=3;

Comment=Additional isoforms seem to exist;

Name=1;

IsoId=P23468-1; Sequence=Displayed;

Name=2; Synonyms=Kidney;

IsoId=P23468-2; Sequence=VSP_005147, VSP_005148, VSP_005149;

Name=3; Synonyms=Retal brain;

IsoId=P23468-3; Sequence=VSP_005150;

-1- PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN

FROM THE TRANSMEMBRANE SEGMENT.

-1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

-1- SIMILARITY: Contains 8 fibronectin type III domains.

-1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.

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EMBL; L38929; AAC41749.1; -.

EMBL; X54133; CAA38068.1; -.

PIR; A56178; A56178.

HSSP; P18052; 1YFO.

Genew; HGNC:9668; PTPRD.

MIM; 601598; -.

GO; GO:0005887; C: integral to plasma membrane; TAS.

GO; GO:0005001; P: transmembrane receptor protein tyrosine pho. . . ; TAS.

GO; GO:0006470; P: protein amino acid dephosphorylation; TAS.

GO; GO:0007185; P: transmembrane receptor protein tyrosine pho. . . ; TAS.

InterPro; IPR008957; FN III-like.

InterPro; IPR003961; FN III.

InterPro; IPR003962; FN III subd.

InterPro; IPR007110; Ig-like.

InterPro; IPR003598; Ig_C2.

InterPro; IPR000387; Tyr_phosphatase.

InterPro; IPR000242; Tyr_PP.

Pfam; PF00041; fn3; 8.

Pfam; PF00047; ig; 3.

Pfam; PF0102; Y_phosphatase; 2.

PRINTS; PR00014; ENTYPRII.

PRINTS; PR00700; PRTYPHPTASE.

SMART; SM00060; FN3; 8.

SMART; SM00408; IGC2; 2.

SMART; SM00194; PTPC; 2.

PROSITE; PS00835; IG LIKE; 3.

PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.

PROSITE; PS00566; TYR_PHOSPHATASE 2; 2.

PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.

Hydrolase; Receptor; Glycoprotein; signal; Transmembrane; Repeat;

Immunoglobulin domain; Alternative splicing.

SIGNAL 1 20

CHAIN 21 1912

DOMAIN 21 1265

PROTEIN-TYROSINE PHOSPHATASE DELTA.

EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 1266 1290 POTENTIAL.
 FT DOMAIN 1291 1912 CYTOPLASMIC (POTENTIAL).
 FT 24 114 IG-LIKE C2-TYPE 1.
 FT DOMAIN 126 224 IG-LIKE C2-TYPE 2.
 FT DOMAIN 236 318 IG-LIKE C2-TYPE 3.
 FT DOMAIN 320 414 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 417 513 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 516 606 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 609 708 FIBRONECTIN TYPE-III 4.
 FT DOMAIN 711 822 FIBRONECTIN TYPE-III 5.
 FT DOMAIN 825 916 FIBRONECTIN TYPE-III 6.
 FT DOMAIN 918 1017 FIBRONECTIN TYPE-III 7.
 FT DOMAIN 1020 1137 FIBRONECTIN TYPE-III 8.
 FT DOMAIN 1375 1618 PROTEIN-TYROSINE PHOSPHATASE 1.
 FT DOMAIN 1619 1912 PROTEIN-TYROSINE PHOSPHATASE 2.
 FT ACT_SITE 1553 PHOSPHOCYSTEINE INTERMEDIATE (BY
 FT ACT_SITE 1844 SIMILARITY).
 FT ACT_SITE 1844 PHOSPHOCYSTEINE INTERMEDIATE (BY
 FT SITE 1175 SIMILARITY).
 FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 724 724 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 832 832 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPPLIC 181 189 Missing (in isoform 2).
 FT VARSPPLIC 226 229 /FTID=VSP_005147.
 FT VARSPPLIC 775 783 Missing (in isoform 2).
 FT VARSPPLIC 609 1137 /FTID=VSP_005148.
 FT MUTAGEN 1178 1178 R->A: 2.5-FOLD REDUCTION IN CLEAVAGE.
 SQ SEQUENCE 1912 AA; 214759 MW; 3AE8CBDCD32182E26 CRC64;

Alignment Scores:
 Pred. No.: 1,39e-48 Length: 1912
 Score: 59.00 Matches: 59
 Percent Similarity: 100.00 Conservative: 0
 Best Local Similarity: 100.00 Mismatches: 0
 Query Match: 5.18% Indels: 0
 DB: 1 Gaps: 0

US-09-719-272-1 (1-3467) x PTPD_HUMAN (1-1912)
 QY 1311 CACATCTGACCAAGCTTCGGAGATGGCGAGGAGAAATGCCACAGTACTGGCCAGCA 1370
 Db 1741 ValMetLeuThrLysLeuArgGluMetGlyArgGluLeuValAspProMetAlaGluTyrAsnMetPro 1760
 QY 1371 GAGCGCTCTGCTCGCTACCAAGTACTTTGTTGTGTACCCGATCGCTGAGTACAACTGCC 1430
 Db 1761 GluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetPro 1780
 QY 1431 CAGTATATCTGCTGAGTTCAGGTCAGGATGCCGGGATGGCGAGTCAAGGACA 1487
 Db 1781 GlnTyrIleLeuArgGluPheLysValThrAspAlaArgAspGlyClnSerArgThr 1799

RESULT 3
 PTNS_HUMAN STANDARD; PRT; 1948 AA.
 ID Q13332; Q15718; Q16341;
 AC Q13332; Q15718; Q16341;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Receptor-type protein-tyrosine phosphatase S precursor (EC 3.1.3.48)
 DE (R-PTP-S) (Protein-tyrosine phosphatase sigma) (R-PTP-sigma).
 GN PTPRS
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Fetal brain;
 RX MEDLINE=96102179; PubMed=8524829;
 RA Pulido R., Serra-Pages C., Tang M., Streuli M.;
 RT "The LAR/PTP delta/PTP sigma subfamily of transmembrane protein-
 tyrosine-phosphatases: multiple human LAR, PTP delta, and PTP sigma
 isoforms are expressed in a tissue-specific manner and associate with
 the LAR-interacting protein LIP-1";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:11686-11690(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96255038; PubMed=8992885;
 RA Endo N., Rutledge S.J., Opas E.E., Vogel R., Rodan G.A., Schmidt A.;
 RT "Human protein tyrosine phosphatase-sigma: alternative splicing and
 inhibition by bisphosphonates";
 RL J. Bone Miner. Res. 11:535-543(1996).
 RN [3]
 RP SEQUENCE OF 1-126 FROM N.A.
 RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
 Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwell S.,
 Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
 Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
 Attix C., Dreiseidner I., Trankheim M., Amico-Keller G., Cosfield J.,
 Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
 Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 Olsen A.S., Carrano A.V.;
 RT "Sequence analysis of a 2.5 Mb region in 19p13.3";
 RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1503-1589 FROM N.A.
 RX MEDLINE=92119637; PubMed=1370651;
 RA Adachi M., Sekiya M., Arimura Y., Takekawa M., Itoh F., Hinoda Y.,
 Imai K., Yachi A.;
 RT "Protein-tyrosine phosphatase expression in pre-B cell NALM-6";
 RL Cancer Res. 52:737-740(1992).
 CC -1- FUNCTION: Interacts with LAR-interacting protein LIP-1.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Comment=Additional isoforms seem to exist;
 CC Name=PTPS;
 CC IsoId=Q13332-1; Sequence=Displayed;
 CC Name=PTPS-MEA;
 CC IsoId=Q13332-2; Sequence=VSP_050021;
 CC Name=PTPS-MEB;
 CC IsoId=Q13332-3; Sequence=VSP_050022, VSP_050026, VSP_050027;
 CC Name=PTPS-MEC;
 CC IsoId=Q13332-4; Sequence=VSP_050024;
 CC Name=PTPS-24-7;
 CC IsoId=Q13332-5; Sequence=VSP_050023, VSP_050025;
 CC -1- TISSUE SPECIFICITY: Detected in all tissues tested except for
 placenta and liver.
 CC -1- SIMILARITY: BELONGS TO THE RECEPTOR CLASS OF THE PROTEIN-TYROSINE
 PHOSPHATASE FAMILY.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domain.
 CC -1- SIMILARITY: Contains 8 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
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 or send an email to license@isb-sib.ch).
 CC EMBL; U35234; AAC50299.1;
 DR EMBL; U40317; AAC50567.1;
 DR EMBL; AC005730; AAC62832.1;
 DR EMBL; S78080; AB221146.2;
 DR HSSP; F18052; LYFO.
 DR Genew; HGNC:9681; PTPRS.

MM; 601576; -- C: integral to plasma membrane; TAS.
GO: 0005887; C: integral to plasma membrane; TAS.
GO: 0005001; F: transmembrane receptor protein tyrosine pho. .; TAS.
InterPro: IPR008957; FN_III-like.
InterPro: IPR003961; FN_III.
InterPro: IPR003962; FN_III subd.
InterPro: IPR007110; IG_c2.
InterPro: IPR003598; IG_c2.
InterPro: IPR000387; TYR_phosphatase.
InterPro: IPR000242; TYR_PP.
Pfam: PF00041; fn3; 8.
Pfam: PF00047; ig; 3.
PRINTS: PR00014; ENTYBELLII.
PRINTS: PR00700; PRTYEPHPTASE.
SMART: SM00600; FN3; 7.
SMART: SM00408; IGC2; 3.
SMART: SM00194; PTPC; 2.
PROSITE: PS00835; IG_LIKE; 3.
PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
PROSITE: PS00056; TYR_PHOSPHATASE_2; 2.
PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 2.
Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
Cell adhesion; Immunoglobulin domain; Alternative splicing; Repeat.
POTENTIAL.
RECEPTOR-TYPE PROTEIN-TYROSINE
PHOSPHATASE S.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
FIBONECTIN TYPE-III 1.
FIBONECTIN TYPE-III 2.
FIBONECTIN TYPE-III 3.
FIBONECTIN TYPE-III 4.
FIBONECTIN TYPE-III 5.
FIBONECTIN TYPE-III 6.
FIBONECTIN TYPE-III 7.
FIBONECTIN TYPE-III 8.
PROTEIN-TYROSINE PHOSPHATASE 1.
PROTEIN-TYROSINE PHOSPHATASE 2.
POLY-PRO.
POTENTIAL.
DISULFID 54 107
DISULFID 156 216
POTENTIAL.
POTENTIAL.
PHOSPHOCYSTEINE INTERMEDIATE (BY
SIMILARITY).
PHOSPHOCYSTEINE INTERMEDIATE (BY
SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
Missing (in isoform PTPS-MEA).
/FTid-VSP_050021.
Missing (in isoform PTPS-MEB).
/FTid-VSP_050022.
Missing (in isoform PTPS-F4-7).
/FTid-VSP_050023.
Missing (in isoform PTPS-MEC).
/FTid-VSP_050024.
V -> I (in isoform PTPS-F4-7).
/FTid-VSP_050025.
Missing (in isoform PTPS-MEB).
/FTid-VSP_050026.
S -> G (in isoform PTPS-MEB).
/FTid-VSP_050027.
T -> HP (IN REF. 2).
SA -> RP (IN REF. 2).
LGPV -> RSPA (IN REF. 2).
GAEGRGPR -> RRARGRRS (IN REF. 2).

FT CONFLICT 910 910 R -> P (IN REF. 2).
FT CONFLICT 986 995 AAEFGANAV -> GLSRARRTL (IN REF. 2).
TV -> SL (IN REF. 2).
F -> S (IN REF. 2).
E -> D (IN REF. 4).
V -> A (IN REF. 4).
N -> K (IN REF. 2).
SQ SEQUENCE 1948 AA; 217080 MW; 7DC049EC03171136 CRC64;
Alignment Scores:
Pred. No.: 1.39e-48 Length: 1948
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
DB: 1 Gaps: 0
US-09-719-272-1 (1-3467) x PTNS_HUMAN (1-1948)
QY 1311 GTCATGCTGACCAAGCTTCGGAGATGGCAGGAGAAATGCCACCACTAGTCCAGCA 1370
DB 1777 ValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAla 1796
QY 1371 GAGGCTCTGCTCCCTACCACTAGTCTTGTGTTGACCCGATGGCTGAGTCAACATGCC 1430
DB 1797 GluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluLysAsnMetPro 1816
QY 1431 CAGTATATCTTCCTGCTGAGTTCACAGTCCAGGATCCCGGATGGCAGTCCAGGACCA 1487
DB 1817 GlnTyrIleLeuArgGluPheLysValThrAspAlaArgAspGlyGlnSerArgThr 1835
RESULT 4
LAR_DROME STANDARD; PRT; 2029 AA.
ID LAR_DROME AC P16621;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase Lar precursor (EC 3.1.3.48) (Protein-
tyrosine-phosphate phosphohydrolase) (DLAR).
GN LAR.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RP SEQUENCE FROM N.A.
RX MEDLINE=90046860; PubMed=2554325;
RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.,
"A family of receptor-linked protein tyrosine phosphatases in humans
and Drosophila.";
Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).
[2]
RP SEQUENCE FROM N.A.
RX STRAIN=Canton-S;
RC MEDLINE=96178473; PubMed=8598047;
RA Krueger N.X., van Vactor D., Wan H.I., Gelbart W.M., Goodman C.S.,
Saito H.,
"The transmembrane tyrosine phosphatase DLAR controls motor axon
guidance in Drosophila.";
Cell 84:611-622(1996).
CC -1- FUNCTION: It is possible that DLAR is a cell adhesion receptor.
It possesses an intrinsic protein tyrosine phosphatase activity
(PTPase). It controls motor axon guidance.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Selectively expressed in a subset of axons and
pioneer neurons in the embryo.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 9 fibronectin type III domains.
CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.


```

DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00194; PTPC: 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS00058; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_2; 1.
DR HYDROLASE.
KW FT DOMAIN
KW FT ACT_SITE 310 310 SER-RICH.
KW FT DOMAIN 327 425 PHOSPHOCYSTEINE INTERMEDIATE (BY
KW FT DOMAIN 382 400 PTPASE INSERT (ASN-RICH).
KW FT DOMAIN 400 POLY-ASN.
KW FT ACT_SITE 521 AA; 59427 MW; OFS16AEDD75EAB96 CRC64;
KW FT SEQUENCE
KW FT SEQUENCE
KW FT SEQUENCE

Alignment Scores:
Pred. No.: 0.00882 Length: 521
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
DB: 1 Gaps: 0

US-09-719-272-1 (1-3467) x PTP1_DICDI (1-521)
QY 309 GGGAGTCACTACATCAATGCCAATCATCATCGATGGC 344
DB 148 GlySerAspTyrIleAsnAlaAsnTyrIleAspGly 159
|||||
|||||

RESULT 7
ID PTPC_MOUSE STANDARD; PRT; 699 AA.
AC P494f6; Q62134; Q62444; Q64496;
DC 01-FEB-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase epsilon precursor (EC 3.1.3.48) (R-PTP-
DE epsilon).
GN PTPRE OR PTPC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID:10090; [1]
RP SEQUENCE FROM N.A.
RP STRAIN:FVB/N;
RC MEDLINE=96064677; PubMed=7592814;
RX Elson A., Leder P.;
RT "Protein-tyrosine phosphatase epsilon. An isoform specifically
RT expressed in mouse mammary tumors initiated by v-Ha-ras or neu."
RL J. Biol. Chem. 270:26116-26122(1995).
RP [2]
RP SEQUENCE FROM N.A.
RP STRAIN=DBA/2;
RC Mukoyama Y.;
RX Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RP [3]
RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6; TISSUE=Brain, and Lung;
RC Hou E.W., Li S.L.;
RX Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RP [4]
RP SEQUENCE OF 224-332 FROM N.A.
RP STRAIN=BALB/c; TISSUE=Brain;
RC MEDLINE=93086603; PubMed=1454056;
RX Schepens J., Zeeuwen P., Wieringa B., Hendriks W.;
RT "Identification and typing of members of the protein-tyrosine
RT phosphatase gene family expressed in mouse brain."
RL Mol. Biol. Rep. 16:241-248(1992).
RP [5]
RP SEQUENCE OF 224-332 FROM N.A.
RP STRAIN=BALB/c; TISSUE=Brain;
RC MEDLINE=95134232; PubMed=7832766;
RX Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;
RT "A novel receptor-type protein tyrosine phosphatase with a single

```

RT catalytic domain is specifically expressed in mouse brain.";
RL Biochem. J. 305:499-504(1995).
CC -|- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC
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CC
CC EMBL; U33688; AAC52281.1; -
DR EMBL; D83484; BAA11297.1; -
DR EMBL; U62387; AAB04553.1; -
DR EMBL; Z23052; CAA80587.1; -
DR EMBL; Z23053; CAA80588.1; -
DR PIR; B61180; B61180.
DR HSSP; P18052; 1YFO.
DR MGD; MGI:97813; Ptpre.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr PP.
DR Pfam; PF00102; Y phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR PHOSPHATASE 1; 2.
DR PROSITE; PS00556; TYR PHOSPHATASE 2; 2.
DR PROSITE; PS00555; TYR PHOSPHATASE_FTP; 2.
KW Glycoprotein; Transmembrane; Hydroxylase; Phosphorylation; Repeat;
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 699 PROTEIN-TYROSINE PHOSPHATASE EPSILON.
FT DOMAIN 20 45 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 46 68 POTENTIAL.
FT TRANSMEM 69 699 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 153 332 PROTEIN-TYROSINE PHOSPHATASE 1.
FT DOMAIN 393 699 PROTEIN-TYROSINE PHOSPHATASE 2.
FT ACT_SITE 334 334 PHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY).
FT ACT_SITE 629 629 PHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY).
FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 500 500 G -> A (IN REF. 2).
FT CONFLICT 506 506 G -> V (IN REF. 2).
FT CONFLICT 521 522 IV -> ML (IN REF. 2).
FT CONFLICT 606 606 M -> I (IN REF. 1).
SQ SEQUENCE 699 AA; 80645 MW; 4D04467438017FEB CRC64;
Alignment Scores:
Pred. No.: 0.00839 Length: 699
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
DB: 1 Gaps: 0
US-09-719-272-1 (1-3467) x PTPSE_MOUSE (1-699)
QY 738 GTGGTGCACTGCAGCGCGGCGTGGCGCCGACCGCG 773
|||
Db 331 ValValHisCysSerAlaGlyValGlyArgThrGly 342
RESULT 8
PTPE HUMAN
ID PTPE_HUMAN STANDARD; PRT; 700 AA.
AC P23469; Q96KQ6;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Protein-tyrosine phosphatase epsilon precursor (EC 3.1.3.48) (R-PTP-
DE epsilon).
GN PTPRE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta;
RX MEDLINE=91006018; PubMed=2170109;
RA Krueger N.X., Struelli M., Saito H.;
RT "Structural diversity and evolution of human receptor-like protein
RT tyrosine phosphatases.";
RL EMBL J. 9:3241-3252(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=22118122; PubMed=12121439;
RA Wabakken T.K., Hauge H., Finne E.F., Wiedlocha A., Aasheim H.C.;
RT "Expression of human protein tyrosine phosphatase epsilon in
RT leucocytes: a potential ERK pathway-regulating phosphatase.";
RL Scand. J. Immunol. 56:195-203(2002).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL -|- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
CC cytoplasmic (isoform 2).
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P23469-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P23469-2; Sequence=VSP_007778;
CC -|- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC
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CC
CC EMBL; X54134; CAA38069.1; -
DR EMBL; AJ315969; CAC86583.1; -
DR EMBL; BC050062; AAH50062.1; -
DR PIR; S12053; S12053.
DR HSSP; P18052; 1YFO.
DR Genew; HGNC:9669; PTPRE.
DR MIM; 600926; -

GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . . ; TAS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR003595; PTPC motif.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR SMART; SM00404; PTPC motif; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE 2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Transmembrane; Hydrolase; Phosphorylation; Repeat;
KW Signal; Alternative splicing.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 700 PROTEIN-TYROSINE PHOSPHATASE EPSILON.
FT DOMAIN 20 46 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 47 69 POTENTIAL.
FT DOMAIN 70 700 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 154 393 PROTEIN-TYROSINE PHOSPHATASE 1.
FT DOMAIN 394 700 PROTEIN-TYROSINE PHOSPHATASE 2.
FT ACT_SITE 335 335 PHOSPHOCYSTEINE INTERMEDIATE (BY
SIMILARITY).
FT ACT_SITE 630 630 PHOSPHOCYSTEINE INTERMEDIATE (BY
SIMILARITY).
FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 70 MEPCPLLVGVSLFLARLGRNETADSNSTTTTSGPPDP
GASQPLALLLLPLLILLLLLAAYFFR -> MSNRSSFS
RLTW (in isoform 2).
FT CONFLICT 516 516 E -> D (IN REF. 2).
FT SEQUENCE 700 AA; 80641 MW; D096BCADCEA65708 CRC64;
Alignment Scores:
Pred. No.: 0.00839 Length: 700
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
DB: 1 Gaps: 0
JS-09-719-272-1 (1-3467) x PTPC_HUMAN (1-700)
2y 738 GTGTGTCAGTCCAGCGGGCGTGGCGGCACCGGC 773
332 ValValHisCysSerAlaGlyValGlyArgThrGly 343
RESULT 9
PTPA RAT
ID PTPA RAT STANDARD; PRT; 796 AA.
AC Q03348;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase alpha precursor (EC 3.1.3.48) (R-PTP-
alpha).
GN PTPA OR LRP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OK NCBI_Taxid=10116;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93038682; PubMed=1417854;
RA Moriyama T., Fujiwara Y., Imai E., Takenaka M., Kawanishi S.,
RA Inoue T., Noguchi T., Tanaka T., Kanada T., Ueda N.;
RT "cDNA cloning of rat LRP, a receptor like protein tyrosine
RT phosphatase, and evidence for its gene regulation in cultured rat
RT mesangial cells."
RL Biochem. Biophys. Res. Commun. 188:34-39(1992).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein

tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L01702; AAA1983.1; -.
DR HSP; P18052; IYFO.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE 2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Transmembrane; Hydrolase; Phosphorylation; Repeat;
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 796 PROTEIN-TYROSINE PHOSPHATASE ALPHA.
FT DOMAIN 20 145 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 146 169 POTENTIAL.
FT DOMAIN 170 796 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 234 494 PROTEIN-TYROSINE PHOSPHATASE 1.
FT DOMAIN 495 796 PROTEIN-TYROSINE PHOSPHATASE 2.
FT ACT_SITE 436 436 PHOSPHOCYSTEINE INTERMEDIATE (BY
SIMILARITY).
FT ACT_SITE 726 726 PHOSPHOCYSTEINE INTERMEDIATE (BY
SIMILARITY).
FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 796 AA; 90260 MW; 4793796191056920 CRC64;
Alignment Scores:
Pred. No.: 0.00821 Length: 796
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
DB: 1 Gaps: 0
US-09-719-272-1 (1-3467) x PTPA_RAT (1-796)
QY 738 GTGTGTCAGTCCAGCGGGCGTGGCGGCACCGGC 773
433 ValValHisCysSerAlaGlyValGlyArgThrGly 444
RESULT 10
PTPA_HUMAN
ID PTPA_HUMAN STANDARD; PRT; 802 AA.
AC P18433; Q14513; Q96TD9;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase alpha precursor (EC 3.1.3.48) (R-PTP-
alpha) OR PTPA.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

SQ SEQUENCE 802 AA; 90599 MW; 8E964C3B5B5B32 CRC64;

Alignment Scores:
 Pred. No.: 0.0082 Length: 802
 Score: 12.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.05% Indels: 0
 DB: Gaps: 0

US-09-719-272-1 (1-3467) x PTR_A_HUMAN (1-802)

QY 738 GTGTCGACTGACGGCGGCGTGGCGGCGACCGGC 773

Db 439 ValValHisCysSerAlaGlyValGlyArgThrgly 450

RESULT 11

ID PTR_A_MOUSE STANDARD; PRT; 829 AA.

AC P18052; Q61808;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-PEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein-tyrosine phosphatase alpha precursor (EC 3.1.3.48) (R-PTP-
 alpha) (LCA-related phosphatase).
 GN PTAPA OR LRP OR PTPA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
 RC STRAIN=C57BL/6 X DBA/2;
 RX MEDLINE=90280391; PubMed=2162042;
 RA Matthews R.J., Cahir E.D., Thomas M.L.;
 RT "Identification of an additional member of the protein-tyrosine-
 phosphatase family: evidence for alternative splicing in the tyrosine
 phosphatase domain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:4444-4448(1990).
 RN [2]
 RP SEQUENCE OF 358-467 FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=95134232; PubMed=7832766;
 RA Hendriks W., Schepens J., Zeeuwen P., Brugman C., Zeeuwen P., Wieringa B.;
 RT "A novel receptor-type protein tyrosine phosphatase with a single
 catalytic domain is specifically expressed in mouse brain.";
 RL Biochem. J. 305:499-504(1995).
 RN [3]
 RP SEQUENCE OF 651-756 FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=93086603; PubMed=1454056;
 RA Schepens J., Zeeuwen P., Wieringa B., Hendriks W.;
 RT "Identification and typing of members of the protein-tyrosine
 phosphatase gene family expressed in mouse brain.";
 RL Mol. Biol. Rep. 16:241-248(1992).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 202-503.
 RX MEDLINE=96320562; PubMed=8700232;
 RA Bilwes A.M., den Hertog J., Hunter T., Noel J.P.;
 RT "Structural basis for inhibition of receptor protein-tyrosine
 phosphatase-alpha by dimerization.";
 RL Nature 382:555-559(1996).
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=P18052-1; Sequences=Displayed;
 CC Name=Short;
 CC IsoId=P18052-2; Sequences=VSP 005146;
 CC -1- TISSUE SPECIFICITY: Widely expressed.
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.

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DR EMBL; M36033; AAA39448.1; -;
 DR EMBL; M36034; AAA39449.2; -;
 DR EMBL; Z23054; CAA80589.1; -;
 DR EMBL; Z23055; CAA80590.1; -;
 DR PIR; A47373; A47373.
 DR PDB; 1YFO; 01-APR-97.
 DR MGD; MGI:97808; Btdra.
 DR InterPro; IPR000367; TYR_phosphatase.
 DR InterPro; IPR000442; TYR_PP.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PRO0700; PRTYPHPTASE.
 DR SMART; SM00194; PTPC; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
 KW Glycoprotein; Transmembrane; Hydrolase; Phosphorylation; Signal;
 KW Repeat; Alternative splicing; 3D-structure.
 FT SIGNAL 1 19 PROBABLE.
 FT CHAIN 20 829 PROTEIN-TYROSINE PHOSPHATASE ALPHA.
 FT DOMAIN 20 142 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 143 166 POTENTIAL.
 FT DOMAIN 167 829 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 232 527 PROTEIN-TYROSINE PHOSPHATASE 1.
 FT DOMAIN 528 829 PROTEIN-TYROSINE PHOSPHATASE 2.
 FT ACT_SITE 469 469 PHOSPHOCYSTEINE INTERMEDIATE (BY
 FT ACT_SITE 759 759 SIMILARITY).
 FT ACT_SITE 759 759 PHOSPHOCYSTEINE INTERMEDIATE (BY
 FT CARBOHYD 21 21 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 51 51 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 80 80 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 104 104 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 124 124 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARSPLIC 268 303 Missing (in isoform Short).
 FT FTIG-VSP 005146.
 SQ SEQUENCE 829 AA; 93697 MW; 7B1E335D4CC809B CRC64;

Alignment Scores:
 Pred. No.: 0.00816 Length: 829
 Score: 12.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.05% Indels: 0
 DB: Gaps: 0

US-09-719-272-1 (1-3467) x PTR_A_MOUSE (1-829)

QY 738 GTGTCGACTGACGGCGGCGTGGCGGCGACCGGC 773

Db 466 ValValHisCysSerAlaGlyValGlyArgThrgly 477

RESULT 12

ID CD45_MOUSE STANDARD; PRT; 1152 AA.

AC P06800;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (lymphocyte
 DE common antigen Ly-5) (CD45) (T200).
 GN PTPRC OR LY-5.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86313686; PubMed=2944116;
RX Saga Y., Tung J.-S., Shen F.-W., Boyse E.A.;
RT "Sequences of Ly-5 cDNA: isoform-related diversity of Ly-5 mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6940-6944(1986).
RN [2]
RP REVISIONS.
RA Saga Y., Tung J.-S., Shen F.-W., Boyse E.A.;
RL Proc. Natl. Acad. Sci. U.S.A. 84:1991-1991(1987).
RN [3]
RP SEQUENCE OF 10-124 FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=86042665; PubMed=3864163;
RA Shen F.-W., Saga Y., Litman G., Freeman G., Tung J.-S., Cantor H.,
RT Boyse E.A.;
RL "Cloning of Ly-5 cDNA";
RN Proc. Natl. Acad. Sci. U.S.A. 82:7360-7363(1985).
RN [4]
RP SEQUENCE OF 822-1152 FROM N.A.
RX MEDLINE=87092355; PubMed=2948186;
RA Raschke W.C.;
RT "Cloned murine t200 (Ly-5) cDNA reveals multiple transcripts within B- and T-lymphocyte lineages";
RL Proc. Natl. Acad. Sci. U.S.A. 84:161-165(1987).
CC -!- FUNCTION: Required for T-cell activation through the antigen receptor. The first PTPase domain has enzymatic activity, while the second one seems to affect the substrate specificity of the first one.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced;
CC Name=1;
CC IsoId=P06800-1; Sequence=displayed;
CC -!- DEVELOPMENTAL STAGE: Expression is restricted to the hematopoietic compartment of development.
CC -!- PTM: Heavily N- and O-glycosylated.
CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.

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DR EMBL; M14342; AAA39458.1; -;
DR EMBL; M15344; AAA39461.1; -;
DR EMBL; M15174; AAA40161.1; -;
DR PIR; A23329; A23329.
DR PIR; A28334; A28334.
DR HSSP; P18052; 1YFO.
DR MGD; MGI:97810; Ptpnc.
DR GO; GO:0005515; P; protein binding; IPI.
DR InterPro; IPR003957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR000387; TYR_PTPase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PTPPHPTASE.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00393; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase; Antigen; T-cell; Repeat; Signal; Transmembrane;
KW Glycoprotein; Phosphorylation; Alternative splicing.
FT SIGNAL 1 23
FT CHAIN 24 1152 LEUCOCYTE COMMON ANTIGEN.
FT DOMAIN 24 425 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 426 447 POTENTIAL.
FT DOMAIN 448 1152 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 233 329 FIBRONECTIN TYPE-III 1.
FT DOMAIN 330 421 FIBRONECTIN TYPE-III 2.
FT DOMAIN 520 769 PROTEIN-TYROSINE PHOSPHATASE 1.
FT DOMAIN 811 1084 PROTEIN-TYROSINE PHOSPHATASE 2.
FT ACT_SITE 701 701 PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).
FT ACT_SITE 1016 1016 PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 318 318 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 379 379 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1152 AA; 130421 MW; B4D956B4E32EA812 CRC64;
Alignment Scores:
Pred. No.: 0.00772 Length: 1152
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.05% Indels: 0
DB: 1 Gaps: 0
US-09-719-272-1 (1-3467) x CD45_MOUSE (1-1152)
QY 738 GTGTCGTCAGTCGAGCGCGTGGCGCGCACCGC 773
Db 698 ValValHisCysSerAlaGlyValGlyArgThrGly 709
RESULT 13
PTNL HUMAN STANDARD; PRT; 1174 AA.
ID PTNL HUMAN
AC Q16825;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 21 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase D1).
GN PTPN21 OR PTPD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=94329538; PubMed=7519780;
RA Moeller N.P.H., Moeller K.B., Lammers R., Kharitonov A., Sures I.,
RL Ullrich A.;
RT "Src kinase associates with a member of a distinct subfamily of protein-tyrosine phosphatases containing an ezrin-like domain";
RL Proc. Natl. Acad. Sci. U.S.A. 91:7477-7481(1994).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein tyrosine + phosphate.
CC -!- SIMILARITY: Contains 1 FERM domain.

CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Non-receptor class subfamily.
 CC -----
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 CC -----
 CC EMBL: X79510; CA56042.1; -
 CC PIR: I38140; I38140.
 CC HSSP: Q06124; 2SHP.
 CC Genew: H9651; PTPN21.
 CC MIM: 603271; -
 CC GO: GO:0005856; C:cytoskeleton; TAS.
 CC GO: GO:0004725; F:protein tyrosine phosphatase activity; TAS.
 CC GO: GO:0006470; P:protein amino acid dephosphorylation; TAS.
 CC InterPro: IPR000299; Band 4.1
 CC InterPro: IPR000387; TYR_phosphatase.
 CC InterPro: IPR000242; TYR_PP.
 CC Pfam: PF00373; Band_41; 1.
 CC Pfam: PF00102; Y_phosphatase; 1.
 CC PRINTS: PR00335; BAND41.
 CC PRINTS: PR00700; PRTYPPHPTASE.
 CC SMART: SM00295; B41; 1.
 CC SMART: SM00194; PTPC; 1.
 CC PROSITE: PS00660; FERM_1; 1.
 CC PROSITE: PS00661; FERM_2; 1.
 CC PROSITE: PS00577; FERM_3; 1.
 CC PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 CC PROSITE: PS00555; TYR_PHOSPHATASE_PTP; 1.
 CC PROSITE: PS00556; TYR_PHOSPHATASE_2; 1.
 CC Structural protein; Cytoskeleton; Hydrolase.
 CC DOMAIN 23 308 FERM.
 CC FT ACT_SITE 921 1174 PROTEIN-TYROSINE PHOSPHATASE.
 CC FT ACT_SITE 1108 1108 PHOSPHOCYSTEINE INTERMEDIATE
 CC (BY SIMILARITY).
 CC FT DOMAIN 340 343 POLY-PRO.
 CC FT DOMAIN 565 574 POLY-PRO.
 CC FT DOMAIN 712 717 POLY-GLU.
 CC SEQUENCE 1174 AA; 133287 MW; 5772D9B1A9B3FDA CRC64;
 Alignment Scores:
 Pred. No.: 0.0077 Length: 1174
 Score: 12.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.05% Indels: 0
 DB: 1 Gaps: 0
 US-09-719-272-1 (1-3467) x PNTL_HUMAN (1-1174)
 QY 1614 GTGCACTGAGTGTGGCGCGGCGGCGG 1649
 Db 1106 VALHSCYSEPALAGLYVALGYARGTHRGIV 1117
 RESULT 14
 PNTL_RAT
 ID PNTL_RAT STANDARD; PRT; 1175 AA.
 AC Q62728; Q62728; (Rel. 35. Created)
 DT 01-NOV-1997 (Rel. 35. Last sequence update)
 DT 10-OCT-2003 (Rel. 42. Last annotation update)
 DE Protein tyrosine phosphatase, non-receptor type 21 (EC 3.1.3.48)
 DE (Protein-tyrosine phosphatase 2E).
 GN PTPN21 OR PTP2E.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxId=10116;
 RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2E).
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=9510449; PubMed=7805871;
 RA U'Abbe D., Banville D., Tong Y., Stocco R., Masson S., Ma S.,
 RA Fanus G., Shen S.H.;
 RT Identification of a novel protein tyrosine phosphatase with sequence
 RT homology to the cytoskeletal proteins of the band 4.1 family.";
 RL FEBS Lett. 356:351-356(1994).
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q62728-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q62728-2; Sequence=VSP 000498;
 CC -1- TISSUE SPECIFICITY: Particularly abundantly in adrenal glands.
 CC -1- SIMILARITY: Contains 1 FERM domain.
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Non-receptor class subfamily.
 CC -----
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 CC -----
 CC EMBL: U17971; AAA62153.1; -
 CC EMBL: U18293; AAA62154.1; -
 CC DR PIR: S51005; S51005.
 CC DR HSSP: Q06124; 2SHP.
 CC DR InterPro: IPR000299; Band 4.1.
 CC DR InterPro: IPR000387; TYR_phosphatase.
 CC DR InterPro: IPR000242; TYR_PP.
 CC Pfam: PF00373; Band_41; 1.
 CC Pfam: PF00102; Y_phosphatase; 1.
 CC PRINTS: PR00335; BAND41.
 CC PRINTS: PR00700; PRTYPPHPTASE.
 CC SMART: SM00295; B41; 1.
 CC SMART: SM00194; PTPC; 1.
 CC PROSITE: PS00660; FERM_1; 1.
 CC PROSITE: PS00661; FERM_2; 1.
 CC PROSITE: PS00577; FERM_3; 1.
 CC PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 CC PROSITE: PS00555; TYR_PHOSPHATASE_PTP; 1.
 CC PROSITE: PS00556; TYR_PHOSPHATASE_2; 1.
 CC Structural protein; Cytoskeleton; Hydrolase; Alternative splicing.
 CC FT DOMAIN 23 308 FERM.
 CC FT ACT_SITE 922 1175 PROTEIN-TYROSINE PHOSPHATASE.
 CC FT ACT_SITE 1109 1109 PHOSPHOCYSTEINE INTERMEDIATE
 CC (BY SIMILARITY).
 CC FT VARSPLIC 1 839 Missing (in isoform 2E).
 CC FT SEQUENCE 1175 AA; 133411 MW; 82A684F1C0F5ECF7 CRC64;
 Alignment Scores:
 Pred. No.: 0.00769 Length: 1175
 Score: 12.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.05% Indels: 0
 DB: 1 Gaps: 0
 US-09-719-272-1 (1-3467) x PNTL_RAT (1-1175)
 QY 1614 GTGCACTGAGTGTGGCGCGGCGGCGG 1649
 Db 1107 VALHSCYSEPALAGLYVALGYARGTHRGIV 1118
 RESULT 15
 PNTL_MOUSE

ID PTNL_MOUSE STANDARD; PRT; 1176 AA.
AC Q62136;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 21 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase PTP-RL10).
GN PTPN21.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=95140431; PubMed=783837;
RA Higashitsugu H., Aril S., Furutani M., Imamura M., Kaneko Y.,
RA Takenawa T., Nakayama H., Fujita T.;
RT "Enhanced expression of multiple protein tyrosine phosphatases in the
RT regenerating mouse liver: isolation of PTP-RL10, a novel cytoplasmic-
RT type phosphatase with sequence homology to cytoskeletal protein
RT 4.1.";
RL Oncogene 10:407-414(1995).
CC -1- FUNCTION: May be involved in the regulation of growth and
CC differentiation of liver cells.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- TISSUE SPECIFICITY: Liver.
CC -1- SIMILARITY: Contains 1 FERM domain.
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.

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DR EMBL; D37801; BAA07053.1; -
DR PIR; I58345; I58345.
DR KSSP; P29350; 1GMZ.
DR MGD; MG1:1344406; Pcpn21.
DR InterPro; IPR000299; Band_4.1.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyk_PP.
DR Pfam; PF00373; Band_41; 1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND41.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00194; PTPc; 1.
DR PROSITE; PS00660; FERM_1; 1.
DR PROSITE; PS00661; FERM_2; 1.
DR PROSITE; PS50057; FERM_3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00385; TYR_PHOSPHATASE_FTP; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR Structural protein; Cytoskeleton; Hydrolyase.
FT DOMAIN 23 308 FERM.
FT DOMAIN 923 1176 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 1110 1110 PHOSPHOCYSTEINE INTERMEDIATE
FT ACT_SITE 1110 1110 (BY SIMILARITY).
FT DOMAIN 340 343 POLY-PRO.
FT DOMAIN 365 372 POLY-PRO.
SQ SEQUENCE 1176 AA; 133490 MW; 529FBE22F1335B75 CRC64;

Alignment Scores:

Pred. No.: 0.00769 Length: 1176
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.05% Indels: 0
DB: 1 Gaps: 0
US-09-719-272-1 (1-3467) x PTNL_MOUSE (1-1176)
QY 1614 GTGCACTGCGAGTGTGCGCGGCGCGCACCGGAGTG 1649
DB 1108 ValHicyserrAlaGlyValGlyArgGlnGlyVal 1119

Search completed: March 9, 2004, 09:04:25
Job time : 72.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 9, 2004, 08:56:18 ; Search time 168 Seconds

(without alignments)
13022.638 Million cell updates/sec

Title: US-09-719-272-1

Perfect score: 1138
Sequence: 1 gattccgactgaagactcc.....atttgataatcagattctc 3467

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2033934

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODE=frame+np_model -DEV=x1p
-Q=/cgn2_1/USPRO.spool_P/US09719272/runat_09032004_085230_7450/app_query.fasta_1.3655
-DB=SPREMBL_25 -QPM=fastan -SUFFIX=spc -MINMATCH=0.1 -LOOFC=0 -LOOPEXT=0
-UNITS=bites -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFM=ptc
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US09719272 @CGN 1.1 188 @runat_09032004_085230_7450 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEOUTRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

1: SPREMBL_25:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_ricent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_rvitus:*
17: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	580	51.0	1191 4	Q723X4 homo sapien

2	506	44.5	1898	4	086WS0	086WS0 homo sapien
3	259	22.8	460	11	062917	062917 rattus norv
4	259	22.8	1887	11	090M67	090M67 rattus sp.
5	254	22.3	1898	11	064604	064604 r protein-t
6	250	22.0	582	11	064696	064696 mus musculu
7	172	15.1	1788	13	091A00	091A00 xenopus lae
8	160	14.1	1898	13	091A07	091A07 mus musculu
9	135	11.9	508	13	090X55	090X55 brachydanio
10	106	9.3	468	13	091B85	091B85 potamorygo
11	59	5.2	140	11	062990	062990 rattus norv
12	59	5.2	192	11	08C922	08C922 mus musculu
13	59	5.2	398	11	062604	062604 rattus norv
14	59	5.2	468	13	091B82	091B82 potamorygo
15	59	5.2	468	13	091B80	091B80 potamorygo
16	59	5.2	615	13	091A18	091A18 xenopus lae
17	59	5.2	749	11	08R169	08R169 mus musculu
18	59	5.2	857	13	090Y74	090Y74 brachydanio
19	59	5.2	1254	11	08VBV0	08VBV0 mus musculu
20	59	5.2	1399	4	075870	075870 homo sapien
21	59	5.2	1499	13	090815	090815 gallus gall
22	59	5.2	1501	11	090W00	090W00 rattus sp.
23	59	5.2	1501	11	07TT17	07TT17 mus musculu
24	59	5.2	1502	4	09UM61	09UM61 homo sapien
25	59	5.2	1863	11	064605	064605 rattus norv
26	59	5.2	1896	13	091A01	091A01 xenopus lae
27	59	5.2	1904	11	064699	064699 mus musculu
28	55	4.8	469	5	09NL11	09NL11 branchiost
29	46	4.0	1231	5	017024	017024 anopheles g
30	45	4.0	1894	11	064487	064487 mus musculu
31	44	3.9	89	4	016343	016343 homo sapien
32	44	3.9	154	11	063847	063847 mus musculu
33	40	3.5	1437	5	044329	044329 hirudo medi
34	38	3.3	469	13	09NL08	09NL08 epistretus
35	34	3.0	383	5	08MTN0	08MTN0 culicoides
36	34	3.0	1597	5	0960M3	0960M3 dirosophila
37	34	3.0	2029	5	09V188	09V188 dirosophila
38	30	2.6	79	11	08CC23	08CC23 mus musculu
39	30	2.6	93	11	08CC54	08CC54 mus musculu
40	25	2.2	468	13	09NL06	09NL06 epistretus
41	25	2.2	472	13	09NL02	09NL02 epistretus
42	25	2.2	2051	5	044328	044328 hirudo medi
43	18	1.6	63	13	090949	090949 gallus gall
44	15	1.3	471	5	09Y1X6	09Y1X6 ephydaria f
45	15	1.3	488	5	09NL12	09NL12 branchiost

ALIGNMENTS

RESULT 1

ID	Q723X4	PRELIMINARY	PRT	1191 AA.
AC	Q723X4			
DT	01-OCT-2003 (TREMBLrel. 25, Created)			
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)			
DE	Hypothetical protein DKFZp686B1310 (Fragment).			
GN	DKFZp686B1310.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISUS-Human cervix;			
RA	Wambutt R., Heubner D., Mewes H.W., Weill B., Amid C., Oeanger A.,			
RA	Popp G., Han M., Wiemann S.,			
RE	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BX537361; CAD97607.1; -			
KW	Hypothetical protein.			
FT	NON_TER			
SO	SEQUENCE	1191 AA;	134914 MW;	8320FEEDDADAC278 CRC64;

Alignment Scores:

Pred. No.: 0 Length: 1191
 Score: 580.00 Matches: 580
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.97% Indels: 0
 DB: 4 Gaps: 0

US-09-719-272-1 (1-3467) x Q723X4 (1-1191)

6 GGACCTGAGAGACCTCTGCTGGCCCACTCTGACCCCTGAGAGATGGAGGCTCAAC 65
 585 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetCysArgLeuAsn 604
 66 TACCAAGACCCCAAGATATGCGAGCAACCCCACTCCCATCCAGCACTGCGGCAAC 125
 605 TyrGlnThrProGlyMetArgAspHisProPheLeuProIleThrAspLeuAlaAspAsn 624
 126 ATCGAGGCGCTCAAAAGCAAGATGGCCCTCAAGTTCTCCAGAGATATGAGTCAATGAC 185
 625 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGlnIleAsp 644
 186 CCTGACAGACAGTTCACGTGGAGATTCAAACTGAGAGTGAACAGCCCAAGACCCG 245
 645 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 664
 246 TATGCGAATGTCATGCGCTTACGACCACTCTGAGATCATCTTACTTATGATGGCGTC 305
 665 TyrAlaAsnValIleLeuAlaThrAspHisSerArgValIleLeuThrSerIleAspIleVal 684
 306 CCCGGAGTGAATCTACATCAATGCCAATCATGATGAGTGAATCCGCAAGCAAGATCCATAC 365
 685 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 704
 366 ATGCGCAAGCAGGCGCCCTGCGCCCAAGACCAATGGCGGATTTTGGAGAAATGGTGGAA 425
 705 IleAlaThrGlnGlyProLeuProGlnThrMetGlyAspPheTrpArgMetValTrpIle 724
 426 CAGCGCAGGCACTGTGTGATGATGACACGCGTGGAGAGAAATCCCGGGTAAAGT 485
 725 GlnArgThrAlaThrValAlaMetCysThrArgLeuGlnGlnLysSerArgValLysCys 744
 486 GATCAGTACTGGCCAGCCCGTGGACCCGAGACCTTGTGCTTATTCAGGTGAACCTGTGTG 545
 745 AspGlnTyrTrpProAlaArgGlyThrGlnThrCysGlyLeuIleGlnValThrLeuLeu 764
 546 GACACAGTGGAGGTGGCCATACATGCTGGGACCTTGGACCTGACCAAGAGTGGCTCC 605
 765 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 784
 606 ACTGAGAACGTTGAGCTGGCTGATTCAGTTTCATGGCTGGCCAGACCATGAGTTGCT 665
 785 SerGlnLysArgGluLeuAlaArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 804
 666 GAGTACCCAACTCCCTGAGCTTCCCTGAGAGCGGGTCAAGGCTTGAACCCCTTAAAC 725
 805 GlnTyrProThrProIleLeuAlaPheLeuArgValLysValCysAsnProLeuAsp 824
 726 GAGAGGCCCATGTTGTCATGACGAGCGGCGTGGCGGCGGACCGGCTGCTTCACTGTG 785
 825 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 844
 786 ATTGATGCCATGTTGAGAGGATGAGACCAAGAAAGCGTGGAAATCTTATGGCCACTGTG 845
 845 IleAspAlaMetLeuAlaArgMetCysHisGlnLysThrValAspIleTyrCysIleVal 864
 846 ACCGTGATCGATCAACAGAGAACTACATGTCGAGACGAGAGCAAGTACGTTTCATC 905
 865 ThrCysMetArgSerIleArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 884
 906 CATGAGCGCTGTGAGGCTGCGACAGTGGCGGCAACAGAGGTGCTCCCGCAACTG 965
 885 HisGlnAlaLeuLeuGlnAlaAlaThrCysGlyHisThrGlnValProAlaArgAsnLeu 904

QY 966 TATGCCCAATCCAGAAAGCTGGGCGCAAGTGCCTCCAGGGAGAGTGTGACCCCATGAG 1025
 DB 905 TyrAlaHisIleGlnLysLeuGlnValProProGlyGlnSerValThrAlaMetGlu 924
 QY 1026 CTGAGATTCAAGTTGCTGGCCAGCTCCAAAGGCCCAACGTCCTGCTTATCAGCGCCAAC 1085
 DB 925 LeuGlnPheLysLeuLeuAlaSerLysAlaHisThrSerArgPheIleSerAlaAsn 944
 QY 1086 CTGCGCTGCAACAGATTCAAGAACCGGCGTGGATGACATGATGCGCTTACAAATGACCCGT 1145
 DB 945 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrCysLeuThrArg 964
 QY 1146 GTGTGTGACGCCATCCGTGTGTGAGAGGCTGTGACTTACATCAATCCAGCTTCTGT 1205
 DB 965 ValCysLeuGlnProIleArgIleValGlnGlySerAspTyrIleAsnAlaSerPheLeu 984
 QY 1206 GATGTTATGACAGAGAGAGGCTTACATGAGTACACAGGGCGCTTGGCAAGAGACCC 1265
 DB 985 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGlnSerThr 1004
 QY 1266 GAGACCTTCTGGCGCATGCTATGGAGACCAATTCACCATCATGTCATGCTGACCAAG 1325
 DB 1005 GluAspPheTrpArgMetLeuTrpGlnHisAsnSerThrIleIleValMetLeuThrLys 1024
 QY 1326 CTTCGGGAGATGGCGAGGAGAAATGCCACAGTACTGGCCGACAGAGCGCTCTGCTGC 1385
 DB 1025 LeuArgGluMetIleTyrGlnLysCysHisGlnTyrTrpProAlaGlnLysSerAlaArg 1044
 QY 1386 TACCAAGATCTTGTGTTTACACCGATGGCTGAGTACACATGCCCAAGTATTCCTGCGT 1445
 DB 1045 TyrGlnTyrPheValValAspProMetAlaGlnTyrAsnMetProGlnTyrIleLeuArg 1064
 QY 1446 GAGTTCAAGTCAACGATGCCGCGGATGGGCGATGAGGCAAGCAATCCGCAAGTTCAGTTC 1505
 DB 1065 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1084
 QY 1506 ACAGACTGGCCAGAGAGAGGCGCGTCCCAAGACAGGCGGAGATTCATGACTTACCTCGG 1565
 DB 1085 ThrAspTrpProGlnGlnValProLysThrGlnGlyGlnPheIleAspPheIleGly 1104
 QY 1566 CAGGTGATTAAGCAAGAGAGAGATTTGAGACAGATGGGCTTATCAGGTCATGCTGCACT 1625
 DB 1105 GlnValHisLysThrLysGlnGlnPheGlnLysAspGlyProIleThrValHisCysSer 1124
 QY 1626 GCTGCGTGGCGCGGACCGGCGGTTCATCACTGAGATGCTCTGAGGCGCATGCGC 1685
 DB 1125 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGlnArgMetArg 1144
 QY 1686 TATGAGGCGGTGTCATGATGTTTCAGACCTGTAAGACCTCGTTCACAGGCTCTGCTGC 1745
 DB 1145 TyrGlnGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 1164

RESULT 2
 ID Q86WS0 PRELIMINARY, PRT, 1898 AA.
 AC Q86WS0;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
 DE Protein tyrosine phosphatase, receptor type, F
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bye;
 RA Strausberg R.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC048768; AA048768.1;
 DR GO; GO:0005634; C:cytosol; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003962; FciliI subd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003598; IG-c2.
DR InterPro; IPR010005; Myb DNA binding.
DR InterPro; IPR003595; PTPC motif.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; FN3; 7.
DR Pfam; PF00047; Ig; 3.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00014; ENTPEI11.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; PTP.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00194; PTPC; 2.
DR SMART; SM00404; PTPC motif; 2.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Receptor.
SQ SEQUENCE 1898 AA; 211673 MW; 034E355624C2PFA7 CRC64;

Alignment Scores:

Pred. No.:	0	Length:	1898
Score:	506.00	Matches:	606
Percent Similarity:	59.84%	Conservative:	0
Best Local Similarity:	99.84%	Mismatches:	1
Query Match:	44.46%	Indels:	0
DB:	4	Gaps:	0

US-09-719-272-1 (1-3467) x Q86MS0 (1-1898)

QY 6 GGACTGAAGAGCTCTTGGCTGGCCCACTCTCTGACCTTGGAGATGCGAGGCTCAAC 65
DB 1292 G1YleuYsaPserLeuAlaHisSerSerAspProValG1uMeCaGArgLeuAsn 1211
QY 66 TACAGAGAGCCAGGATGTCGAGACACACCCATCCCATCAACGAGCTGGAGCAAC 125
DB 1312 TyGlnThrProG1yMeValArgAspHisProProIleProIleThrAspLeuAlaAspAsn 1331
QY 126 ATCGAGCGCTCAAGCCACGATGGCTCAAGTTCTCCAGAGATGAGTCCATGAC 185
DB 1332 I1eG1uArgLeuYsa1aAsnAspG1yLeuYsaPserSerG1ng1uYrG1uSer11eAsp 1351
QY 186 CCTGGACAGCAGTTCACGTGGGAGATTCAACTGGAGGTGAACAAGCCCAAGACCGC 245
DB 1352 ProG1yG1ng1uInPheThr1rPgluAsnSerAsnLeuG1uValAsnYsaProLYsaAsnArg 1371
QY 246 TATCGAATGTCATGCTGCTTACGACCACTTGGAGTCACTTACCTTATCATGAGCGTC 305
DB 1372 Tyr1aAsnVal11eAla1yAspHisSerArgVal11eLeuThrSer11eAspG1yVal 1391
QY 306 CCGGAGAGTGACTCATCATGATGCAATGCAATCATCATGATGCTTACCGCAGAGATGCTTAC 365
DB 1392 ProG1ySerAspYr11eAsnAlaAsnYr11eAspG1yYrArg1yG1uAsnAla1yYr 1411
QY 366 ATCGCAGCAGAGGCGCCCTTCCGAGAGCATGGGCGATTTCTGGAGATGCTGGAGAA 425
DB 1412 Thr1aThrG1ng1uProLeuProG1uThrMetG1yAspPhe1rPaGmetVal1rPglu 1431
QY 426 CAGGCAAGCGGCACTGTGCTCATGATGACAGCGCTGAGAGAGAGTCCCGGSTRMAATGT 485
DB 1432 G1nArgThrAlaThrAlaValaValaMetMetThrArgLeuG1uG1uYsaSerArgValaYsa 1451
QY 486 GATCATGATGTCAGAGCGCCGTGGACCGAGACCTGTGAGCTTATTCAGTGAACCTGTGG 545

DB 1452 AspG1n1yTrpProAlaArgG1yThrG1uThrCySg1yLeu11eG1nValThrLeuLeu 1471
QY 546 GACACAGTGGAGCTGGCCCAATCACTGTGGGCACTTGGACATCCACAAGAGTGGCTCC 605
DB 1472 AspThrValG1uLeuAlaThrYrThrValArgThrPheAlaLeuHis1ySer1ySer 1491
QY 606 AGTGAAGAGCTGAGCTGGCTGATGTTCAAGTTCATGAGCTGGCGAGACCAAGAGATTGCT 665
DB 1492 SerG1uYsaArgG1uLeuArgG1uInPheMetAla1rProAspHisG1yValPro 1511
QY 666 GAGTACCAACTCCCATCTTGGCTTCTTACAGCGGTCGAAGGCTTGAACCCCTTAAC 725
DB 1512 G1uYrProThrProIleLeuAlaPheLeuArgValaG1yValaCyAsnProLeuAsp 1531
QY 726 GAGAGGCCATGTGTGCACTGACGCGCGGCGGCGCCCAACCGCTGCTTACGCTG 785
DB 1532 AlaG1yPrometValaValaHisCySerAlaG1yValaG1yArgThrG1yCySPhe11eVal 1551
QY 786 ATTGATGCCATGTTGAGAGCGGATGAGACAGAGAAAGCGTGGACATTTATGCCACGTG 845
DB 1552 11eAspAlaMetLeuG1uArgMetYsaHisG1uYsaThrValaAsp11eYrG1yHisVal 1571
QY 846 ACTCGATGCGATCAAGAGAGAACTACATGAGGAGAGAGAGACAGTACGTGTTCATC 905
DB 1572 ThrCyMetArgSerG1nArgAsnYrMetValG1nThrG1uAspG1nYrValaPhe11e 1591
QY 906 CATGAGCGCTGCTGAGAGCTTCCACGTGCGGCGCCACAGAGAGTCCCGCCGCAACCTG 965
DB 1592 HisG1uAla1eLeuG1uAla1a1aThrCySg1yHisThrG1uValProAlaArgAsnLeu 1611
QY 966 TATGCCCATTCACAGAACTGGGCGCAATGCTCCAGGAGAGAGTGAACCGCATGAG 1025
DB 1612 TyrAlaHis11eG1nYsaLeuG1yG1nValaProProG1yG1uSerValThrAlaMetC1u 1631
QY 1026 CTCGAGTTCAGAGTCTGCTGCGGAGCTTCAAGGCCCAACAGTCCGCTTCATCAGGCGCAAC 1085
DB 1632 LeuG1uInPheYsaLeuLeuAlaSerSerYsaHisThrSerArgPhe11eSerAlaAsn 1651
QY 1086 CTGCGCTGCAACAATTCAGAAACCGGCTGGTGAACATCAAGCCCTAGATGACCGGT 1145
DB 1652 LeuProCyAsnLYsaPheLYsaAsnArgLeuValaSn11eMetProYrG1uLeuThrArg 1671
QY 1146 GTGTGTGAGAGCCCATCGAGTGTGAGAGGAGCTCTGACTCATCAATGAGCTTCCGT 1205
DB 1672 ValCySleuG1nProIleArgG1yValG1uG1ySerAspYr11eAsnAlaSerPheLeu 1691
QY 1206 GATGTTATGACAGACAGAGGCTTCAATAGCTACAGAGGCGCTTGGCAGAGACACC 1265
DB 1692 AspG1yYrArgG1ng1uYsaAlaYr11eAlaThrG1ng1yProLeuAlaG1uSerThr 1711
QY 1266 GAGGACTTGGCGCATGCTATGGAGAGCAATTCACATCATGCTGATGACCAAG 1325
DB 1712 G1uAspPhe1rPaGmetLeu1rPgluHisSerSerThr11e11eValaMetLeuThr1yS 1731
QY 1326 CTTCGAGAGATGGAGAGAAATGCCACAGATCTGGCAGAGAGCGCTGCTGCG 1385
DB 1732 LeuArgG1uMetG1yArgG1uLYsaHisG1nYr1rPProAlaG1uArgSerValaArg 1751
QY 1386 TACAGTACTTGTGTTGACCCGATGGCTAGTGAACAATGCGCCAGTATATCTGGGT 1445
DB 1752 TyrG1nYrPheValaValaAspPrometAlaG1uYrAsmetProG1nYr11eLeuArg 1771
QY 1446 GAGTTCAGAGTCAAGATGCGCGGATGGGAGTCAAGAGAAATCCGCACTTCCAGTTC 1505
DB 1772 G1uPheLYsaVal1rAspAlaArgAspG1yG1nSerArgThr11eArgG1nPhG1nPh 1791
QY 1506 AGAGCTGCGCAGAGCAGGCGGTGCCCAAGCAGGCGAGGATCATTTGATGATGGGG 1565
DB 1792 ThrAspThrProG1uG1ng1yValaProLYsaThrArg1yG1uG1yPhe11eAspPhe11eG1y 1811
QY 1566 CAGGTGATTAAGCAACAGAGCAAGTTCAGAGATGGGCTTATCAAGTGCAGTGCAGT 1625


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Db      1812 GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1831
QY      1826 GCTGGCGTGGCGCCGACCGGGGTGTTCATCATCTTGAGCATGCTCTGAGCGCATGGC 1685
Db      1832 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 1851
QY      1886 TATATAGGGCGGTGGTGCATGTTTCAGACCGTGAAGACCTGGCGTACACAGCGTCTGGCC 1745
Db      1852 TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnAlaGlyProAla 1871
QY      1746 ATGTGTGACAGACAGACGACCATATCAAGTGTGCTACCGTGGCGCTTGAGTACTTGGC 1805
Db      1872 MetValGlnThrGluAspGlnTyrGlnLeuGlyTyrArgAlaIleAlaLeuGluTyrLeuGly 1891
QY      1806 AGCTTTGACCATATGCAACG 1826
Db      1892 SerPheAspHisTyrAlaThr 1898

RESULT 3
ID      062917      PRELIMINARY;      PRT;      460 AA.
AC      062917.
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT      01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE      IAR receptor-linked tyrosine phosphatase.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_Taxid=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Sprague Dawley; TISSUE=Brain;
RX      MEDLINE=94075340; PubMed=8253779;
RA      Longo F.M., Martignetti J.A., Le Beau J.M., Zhang J.S., Barnes J.P.,
RA      Brosius J.
RT      "Leukocyte common antigen-related receptor-linked tyrosine
RT      phosphatase. Regulation of mRNA expression."
RL      J. Biol. Chem. 268:26503-26511(1993).
DR      EMBL; U00477; AAC04306.1; -.
DR      PIR; A56493; A56493.
DR      HSSP; P18052; 1YFO.
DR      GO; GO:0016787; F:hydrolase activity; IEA.
DR      GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR      InterPro; IPR000387; Tyr_P.
DR      InterPro; IPR000242; Tyr_PP.
DR      Pfam; PF00102; Y_phosphatase; 2.
DR      PRINTS; PR00700; ERTYHPHPTASE.
DR      SMART; SM00194; FTRP; 2.
DR      PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR      PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
DR      PROSITE; PS00055; TYR_PHOSPHATASE_FTP; 2.
KW      Hydrolase; Receptor.
SQ      SEQUENCE 460 AA; 52989 MW; B78C8E504F1260FA CRC64;

Alignment Scores:
Pred. No.:      1,13e-256      Length:      460
Score:      259.00      Matches:      259
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      22.76%      Indels:      0
DB:      11      Gaps:      0

US-09-719-272-1 (1-3467) x 062917 (1-460)
QY      1050 TCAGAGCCCAACAGCTCCGCTTCATATAGCGCCCACTGCGCTGCAACAAGTTCAGAGAC 1109
Db      202 SerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysAlnLysPheLysAsn 221
QY      1110 CGGCTGTGAACATCATGCGCTCAAGATTACCGCGTGTGTGTGTGAGGCCATCCCTGTGT 1169

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Db      222 ArgLeuValAsnIleMetProTyrGluLeuThrArgValLysLeuGlnProIleArgGly 241
QY      1170 GTGAGGGCTCTGACTCATCATATGACAGCTTCCTGATGGTTATAGACAGACAGAGGCC 1229
Db      242 ValGluGlySerAspTyrIleAsnHisSerPheLeuAspGlyTyrArgGlnGlnLysAla 261
QY      1230 TACATAGCTACACAGGGCGCTCTGGCAGAGACCCAGAGACTTCTGGCGCATGCTTGG 1289
Db      262 TyrIleAlaThrGlnGlnGlyProLeuAlaGluSerThrGluAspPheTrpArgMetLeuTrp 281
QY      1290 GAGCAATTCACCATCATGTCATGTCATGTCAGAGCTCGGAGATGGGACAGAGAAA 1349
Db      282 GluHisAsnSerThrIleIleValMetLeuThrLysLeuArgGluMetGlyArgGluLys 301
QY      1350 TGCCACAGTACTGGCCGACAGAGCGCTCTGCTGCTACCACTTCTTTGTTGACCCG 1409
Db      302 CysHisGlnTyrTrpProAlaGluArgSerAlaArgTyrGlnTyrPheValAlaAspPro 321
QY      1410 ATGGCTGAGTACAAATGCGCCAGATATCTGGGTGAGTCAAGTCAAGTCAGATGCCCG 1469
Db      322 MetAlaGluTyrAsnMetProGlnTyrIleLeuArgGluPheLysValThrAlaAlaArg 341
QY      1470 GATGGGAGTCAAGACATCCGAGGATTCACAGTTCACAGACTGGCCAGACAGGCGCTG 1529
Db      342 AspGlyGlnSerArgThrIleArgGlnPheGlnPheThrAspTrpProGluGlnGlyVal 361
QY      1530 CCCAGACAGGCGAGGATTCATTGACTTCATCGGGGAGGAGCATTAAGACCAAGAGCAG 1589
Db      362 ProLysThrGluGlnGlyPheIleAspPheIleGlyGlnValHisLysThrLysGluGln 381
QY      1590 TTGTGACAGAGATGGGCTCATCAAGTGTGACTGACATGCTGCGGTGGCGGCGGCGGTG 1649
Db      382 PheGlyGlnAspGlyProIleThrValHisCysSerAlaGlyValArgThrGlyVal 401
QY      1650 TTCATCATCTGACATGCTCTCTGAGAGGCGATGCGCTTGAAGGGGTGGTGACATGTT 1709
Db      402 PheIleThrLeuSerIleValLeuGluArgMetArgTyrGluGlyValValAspMetPhe 421
QY      1710 CAGACCGTGAAGACCTGGGTGACAGAGCTCTGTCATGTTGACAGACAGAGACAGAT 1769
Db      422 GlnThrValLysThrLeuArgThrGlnArgProAlaMetValGlnThrGluAspGlnTyr 441
QY      1770 CAGCTGTGCTACCGTGGCGGCTTGAGTACTCTGGCAGCTTGAACCATATGCAACG 1826
Db      442 GlnLeuGlyTyrArgAlaIleAlaLeuGluTyrLeuGlySerPheAspHisTyrAlaThr 460

RESULT 4
ID      09067      PRELIMINARY;      PRT;      1887 AA.
AC      09067.
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE      IAR, leukocyte common antigen-related PROTEIN=TRANSMEMBRANE receptor
DE      phosphotyrosine phosphatase.
OS      Rattus sp.
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_Taxid=10118;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      MEDLINE=92278755; PubMed=1317540;
RX      Yu Q., Lemario T., Weinberg R.A.;
RT      "The N-terminal and C-terminal domains of a receptor tyrosine
RT      phosphatase are associated by non-covalent linkage."
RL      Oncogene 7:1051-1057(1992).
DR      HSSP; P18052; 1YFO.
DR      GO; GO:0005634; C:nucleus; IEA.
DR      GO; GO:0003677; F:DNA binding; IEA.
DR      GO; GO:0016787; F:hydrolase activity; IEA.
DR      GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR      GO; GO:0006470; F:protein amino acid dephosphorylation; IEA.
DR      InterPro; IPR003962; FcIITL_subd.

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CC IsoId=Q64604-2; Sequence=VSP_050409, VSP_050410, VSP_050413,
 CC Name=PLIAR4.0;
 CC IsoId=Q64604-3; Sequence=VSP_050415;
 CC Name=PLIAR18.1;
 CC IsoId=Q64604-4; Sequence=VSP_050414, VSP_050415;
 CC Name=PLIARCB9;
 CC IsoId=Q64604-5; Sequence=VSP_050411, VSP_050412;
 CC TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEURAL OR
 CC NEUROSCUTULAR TISSUE.
 CC -1 TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEURAL OR
 CC NEUROSCUTULAR TISSUE.
 CC -1 DEVELOPMENTAL STAGE: THE ALTERNATIVELY SPLICED ISOFORMS ARE
 CC DEVELOPMENTALLY REGULATED
 CC -1 SIMILARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (3 IG-LIKE
 CC DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS), AND A
 CC CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS (BY SIMILARITY).
 DR EMBL; L11586; AAC37655.1; -
 DR EMBL; M60103; AAA41510.1; -
 DR EMBL; X83505; CAA58495.1; -
 DR EMBL; X83546; CAA58537.1; -
 DR PIR; S46215; S46216.
 DR HSSP; F18052; 1YFO.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0005194; F:cell adhesion molecule activity; IEA.
 DR GO; GO:0016787; F:hydroxylase activity; IEA.
 DR GO; GO:0004727; F:phosphatidylserine phosphatase act. .; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007155; F:cell adhesion; IEA.
 DR GO; GO:0006700; F:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003962; FNIII_subd.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_C2.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; TYR_PP.
 DR Pfam; PF00041; fn3; 7.
 DR Pfam; PF00047; 1g; 3.
 DR Pfam; PF0102; Y_phosphatase; 2.
 DR PRINTS; PR00014; ENTPEP11.
 DR PRINTS; PR00700; PRTPHPHTASE.
 DR SMART; SM00060; FN3; 6.
 DR SMART; SM00408; IG_C2; 2.
 DR SMART; SM00194; PTPC; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 KW Hydroxylase; Receptor; Glycoprotein; Signal; Transmembrane;
 KW Cell adhesion; Immunoglobulin domain; Alternative splicing; Repeat.
 FT CHAIN 1 27
 FT SIGNAL 1 27
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QY 1617 CACTGAGTCTGACGCGGCGCCACCGGGGTTCATCACTCTGAGCATCGCTGAG 1676
 Db 513 HicyserraliaglyalglargthrglyalPheillethreusertilevalleuglu 532
 QY 1677 CGATGCGCTATGAGGGCGGTGTCGACATGTTTCAACCGGTGAAGCCCTGGTACAG 1736
 Db 533 ArgMeerArgTylgluglyalValaspMetPheglInthrValylThrleuArgThrgIn 552
 QY 1737 CGTCTGCGCATGGTGACAGACAGACAGATGATCACTGCTGCTACCGTGGCCCTGAG 1796
 Db 553 ArgProhlaMetvalglInthrgluaSpglInthrleuCyserYrarglaalaaleuglu 572
 QY 1797 TACCTGCGACGCTTTGACCACTATGCAACG 1826
 Db 573 TyrlenglyserPheaspHisTyrAlaThr 582

RESULT 7

Q91AJ0 PRELIMINARY; PRT; 1788 AA.

AC Q91AJ0; 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Receptor protein tyrosine phosphatase IAR.
 GN XPRP-IAR.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20193505; PubMed=10727868;
 RA "Johnson K.G., Holt C.E.;
 RT "Expression of Crp-alpha, IAR, PTP-delta, and PTP-rho in the
 RT developing xenopus visual system.";
 RL Mech. Dev. 92:291-294(2000).
 DR HSSP; AF:97945; AAF43606.1; -.
 DR HSSP; P18052; IYFO.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR008957; FN_III.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR007110; IG_II-like.
 DR InterPro; IPR003598; IG_C2.
 DR InterPro; IPR000387; Tyr_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; Fn3; 7.
 DR Pfam; PF00047; Ig; 3.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR SMART; SMO0060; FN3; 7.
 DR SMART; SMO0408; IG2; 3.
 DR SMART; SMO0194; PTPC; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 KM Hydrolase; Immunoglobulin domain; Repeat.
 SQ SEQUENCE 1788 AA; 200271 MW; AB19254986D9067 CRC64;

Alignment Scores:

Pred. No.: 3,34e-167 Length: 1788
 Score: 172.00 Matches: 172
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 15, 11% Indels: 0
 DB: 13 Gaps: 0

US-09-719-272-1 (1-3467) X Q91AJ0 (1-1788)

QY 1311 GTCATGCTGACCAAGCTTCGGAGATGGGAGAGAGAAATGCCACCAAGTACTGGCAGCA 1370

Db 1617 ValMetleuthrYlsleuArgGlumeGlyArgGlulyseshleuglIntrProAla 1636
 QY 1371 GAGGCTCTGCTGCTACCAAGTACTTGTGTGACCCGATGAGTGAACAACAGCC 1430
 Db 1637 GlurserAlaargYrglIntrYrPheValValaspPronetAlaIntrYrMetPro 1656
 QY 1431 CAGTATATCTGCGTGAAGTTCAAGTCAACGATGCCGAGATGGGAGTCAAGACAATC 1490
 Db 1637 GlIntrYrleuArgGluphelysValThrAspAlaargspglYglInserArgThrIle 1676
 QY 1491 CGGAGTTTCCAGTTCAACAGTCCGACGACGAGGCGTCCCAAGACGAGGATTC 1550
 Db 1677 ArgInPheglInPheIntrAspTrpProglngInglyAlaProlystrglYgluglyPhe 1696
 QY 1551 ATTGACTTCATCGGCGAGGTGATAGACCAACAGAGAGAGTTTGACAGATGGCCCTATC 1610
 Db 1697 IleaspheIlelglYglInValHslYsThrlyglInglInPheglYglInspglYProIle 1716
 QY 1611 ACGGTGACATGTCATCTGCGCGTGGCCGACCCGAGGTGTTCATCACTCTGACATCTC 1670
 Db 1717 ThrValHscyserraliaglyalglYargthrglyalPheillethreusertileval 1736
 QY 1671 CTGAGAGCGCATGCGCTATGAGCGGTGTCGACATGTTTCAACCGGTGAAGCCCTGCGT 1730
 Db 1737 leugluargMetargYrgluglyalValaspMetPheglInthrValylThrleuarg 1756
 QY 1731 ACACAGCGTCTGCGCATGTCGACAGACAGACAGATATCACTGTGCTACCGTGGCGCC 1790
 Db 1757 ThrglIntrProhlaMetvalglInthrgluaSpglInthrleuCyserYrarglaala 1776
 QY 1791 CTGAGTACCTCGGACGCTTTGACCACTATGCAACG 1826
 Db 1777 leugluYrleuglyserPheaspHisTyrAlaThr 1788

RESULT 8

Q9EQ17 PRELIMINARY; PRT; 1898 AA.

AC Q9EQ17; 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Tyrosine phosphatase IAR.
 GN PTPRF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RX MEDLINE=21135493; PubMed=11241288;
 RA Terzowski G., Jankowski A., Hendriks W.J.A.J., Rolink A.G.,
 RA Kistelow P.;
 RT "Within the hemopoietic system, IAR phosphatase is a T cell lineage-
 RT specific adhesion receptor-like protein whose phosphatase activity and
 RT appears dispensable for T cell development, repertoire selection and
 RT function.";
 RL Eur. J. Immunol. 31:832-840(2001).
 DR HSSP; AF300943; AAG40194.1; -.
 DR HSSP; P18052; IYFO.
 DR MGD; MGI:102695; PTPRF.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003962; FNIII_subd.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR007110; IG_II-like.
 DR InterPro; IPR003598; IG_C2.
 DR InterPro; IPR000387; Tyr_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; Fn3; 7.
 DR Pfam; PF00047; Ig; 3.

DR Pfam: PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00014; FNTYPRIT.
 DR PRINTS: PR00700; PRTYPRHTASE.
 DR SMART: SM00406; FN3; 6.
 DR SMART: SM00408; IG2; 2.
 DR SMART: SM00194; PTPC; 2.
 DR PROSITE: PS50835; IG LIKE; 3.
 DR PROSITE: PS50833; TYR_PHOSPHATASE_1; 2.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
 DR Hydrolyase; Immunoglobulin domain; Repeat.
 KW SEQUENCE 1898 AA; 211504 MW; EPD48DD1B352A4A CRC64;

Alignment Scores:

Pred. No.:	7,456-155	Length:	1898
Score:	160.00	Matches:	160.
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	14.06%	Indels:	0
DB:	11	Gaps:	0

US-09-719-272-1 (1-3467) x Q90YJ5 (1-1898)

QY	1077	AGCGCCAACTCCCTCGACCAAGTTCAGAACCGCGTGGGAACATCATGCGCTAGGA	1136
DB	1649	SerialaenLeupProCyAsnlysephelysasnlrgLeuValaenlleMeleProtyGlu	1668
QY	1137	TTGACCCGTGTGTCTCGACGCCATCCGTGTGTGAGGGCTCTGACTCATCATGATGCC	1196
DB	1669	LeuthlrarGvalCyLeuGlnProIleargGlyValGlnGlySerarPtyrilleAsnAla	1688
QY	1197	AGCTTCTCGATGTTATAGACAGAAAGCTTCATAGCTACACAGGGGCTCTGGCA	1256
DB	1689	SerPheleuasPglYrArgGlnGlnlysalYrilleaIatngInglyProleuAla	1708
QY	1257	GAGACACCGACAGACTTCCTGGGCGATGCTATGGAGACAAATCCACCATCATGCTATG	1316
DB	1709	GlnserThnGluasPheThraPrgmetLeutrgIwhIsenserThilleleValMet	1728
QY	1317	CTGACCAAGCTTCGGAGATGGGCAAGGAGAAATGCCACGACTGCGCCAGAGAGCG	1376
DB	1729	LeuthrlyLeuargGluMetGlyArgGlnlyscYshIsGlnlyYrPrAlaGluArg	1748
QY	1377	TGTGTCCTACAGACTTGTGTGACCGGATGGCTGAGTCAACATGCGCCAGAT	1436
DB	1749	SerAlaArgYrGlnlyrPheValValaPhePrometAlaGlnlyrAsnMetProGlnlyr	1768
QY	1437	ATCTGCTGAGTTCAGAGTACGAGATGCCCGGATGGGCACTCAAGCAATCCGCGAG	1496
DB	1769	IleleuArgGluPheleValThrAspAlaArgAspGlyGlnSerArgThrilleArgGln	1788
QY	1497	TTCCAGTTCACAGACTGGCGACAGACGGCGTGGCCCAAGACAGCGAGGAGATTCTTAC	1556
DB	1789	PheGlnPheThraPrgProGlnGlnlyValProlysthnGlyGlnGlyPheIleAsp	1808

RESULT 9

Q90YJ5 PRELIMINARY; PRT; 508 AA.

AC Q90YJ5; PRELIMINARY; PRT; 508 AA.
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Receptor protein-tyrosine phosphatase IAR (Fragment).
 GN PTPRP OR IAR.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RA SEQUENCE FROM N.A.
 RA van der Sar A., Berist M., de Fockert J., Overvoorde J., Zivkovic D.,
 RA den Hertog J.;

RT "Expression of receptor protein-tyrosine phosphatase alpha, sigma and
 RT IAR during development of the zebrafish embryo."
 RT Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 RL EMBL; AJ311885; CAC44758.1; -
 DR ZFIN; ZDB-GENE-020107-2; ptpf.
 DR GO; GO:0016787; P:hydrolase activity; IEA.
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; TYR_PP.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS: PR00700; PRTYPRHTASE.
 DR SMART; SM00194; PTPC; 2.
 DR PROSITE; PS50833; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
 KW Hydrolyase.
 FT NON TER

Alignment Scores:

Pred. No.:	4,796-129	Length:	508
Score:	135.00	Matches:	135
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	11.86%	Indels:	0
DB:	13	Gaps:	0

US-09-719-272-1 (1-3467) x Q90YJ5 (1-508)

QY	1311	GTCATGCTGACCAAGCTTCGGAGATGGGCAAGGAGAAATGCCACAGTACTGGCGACA	1370
DB	337	ValMetLeuThrlyLeuargGluMetGlyArgGlnlyscYshIsGlnlyrPrgProAla	356
QY	1371	GAGCGCTCTGCTGCTACCAAGTTCCTGTTGACCCGATGGCGAGTACAAATGGCC	1430
DB	357	GluArgSerAlaArgYrGlnlyrPheValValaPhePrometAlaGlnlyrAsnMetPro	376
QY	1431	CAGTATATCTCGGTGAGTTCAGAGTTCAGATGCCCGGATGGGCACTGCAAGCAATC	1490
DB	377	GlnlyrIleleuargGluPheleValThrAspAlaArgAspGlyGlnSerArgThrille	396
QY	1491	CGGCACTTCAGTTCACAGACTGGCCAGACAGGGCGTCCCAAGACAGCGAGGATTC	1550
DB	397	ArgGlnPheGlnPheThraPrgProGlnGlnlyValProlysthnGlyGlnGlyPhe	416
QY	1551	ATTGACTTCATGGGCGAGGTGACCAAGACAGCAAGTTCAGAGGATGGGCTATC	1610
DB	417	IleasPheIleleValValaHsluYsthnlyscYshIsGlnPheGlyGlnAspGlyProIle	436
QY	1611	ACGGTGCATCGAGTCTGGCGTGGCCGACCGGGGTTCATCACTCTGAGCATCGTC	1670
DB	437	ThrValHisCyserAlaGlyValGlyArgGlnlyValPheIleThrIleuSerIleVal	456
QY	1671	CTGAGAGCATGGGCTATGAGGGCGTGGTGCATGTTTCAGACC	1715
DB	457	LeuGluArgMetArgYrGlnlyValValaPheMetPheGlnThr	477

RESULT 10

Q91BA5 PRELIMINARY; PRT; 468 AA.

AC Q91BA5; PRELIMINARY; PRT; 468 AA.
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE RYPTPR2Aa protein (Fragment).
 GN RYPTPR2Aa.
 OS Potamotrygon moroco (South American freshwater stingray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Rhammobranchii; Squalae; Hymnosquales; Pristiorhina; Batoidae;
 OC Myliobatiformes; Myliobatoidae; Potamotrygonidae; Potamotrygon.
 OX NCBI_TaxID=86373;
 RN [1]

FT NON TER 1 1
 SQ SEQUENCE 192 AA; 22551 MW; B78B194500F33B1A CRC64;
 Alignment Scores:
 Pred. No.: 9.18e-51 Length: 192
 Score: 59.00 Matches: 59
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.18% Indels: 0
 DB: 11 Gaps: 0
 US-09-719-272-1 (1-3467) x Q8C922 (1-192)
 QY 1311 GTCATGCTGACCAAGCTTCGGAGATGGCGAGGAGAAATGCCACAGTACTGGCCAGCA 1370
 Db ValmetLeuthrLysLeuArgLysGluMetGlyArgGluLysCySHsgIntYrTTPProAla 40
 QY 1371 GAGGCTCTGCTGCTACCAAGTACTTTGTTTACCCGATGGCTGAGTACAAATGCC 1430
 Db GlutArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGlnTyrAsnMetPro 60
 QY 1431 CAGTATATCTGCGCTGAGTTCAAGGTACCGGATGCCGGATGGCGAGTCAAGGACA 1487
 Db GlnTyrIleLeuArgLysGluPheValThrAspAlaArgAspGlyGlnSerArgThr 79
 RESULT 13
 ID Q62604 PRELIMINARY; PRT; 398 AA.
 AC Q62604;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN CPrp1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STEIN=Sprague Dawley; TISSUE=Occipital cortex;
 RX MEDLINE=94045925; PubMed=8229209;
 RA Sahin M., Hockfield S.;
 RT "Protein tyrosine phosphatases expressed in the developing rat
 brain.";
 RL J. Neurosci. 13:4968-4978(1993).
 DR EMBL; U03273; AAC52124.1; -.
 DR PIR; I56540; I56540.
 DR HSP; P18052; LYFO.
 DR GO; GO:0016787; P:hydrolase activity; IEA.
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; TYR_PP.
 DR Pfam; PF00102; Y_PTPase.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00194; PTPC; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_2; 2.
 KM Hypothetical protein; Hydrolase.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 398 AA; 45618 MW; AYCAB3AE6D589E17 CRC64;
 Alignment Scores:
 Pred. No.: 8.34e-51 Length: 398
 Score: 59.00 Matches: 59
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.18% Indels: 0
 DB: 11 Gaps: 0

US-09-719-272-1 (1-3467) x Q62604 (1-398)
 QY 1311 GTCATGCTGACCAAGCTTCGGAGATGGCGAGGAGAAATGCCACAGTACTGGCCAGCA 1370
 Db ValmetLeuthrLysLeuArgLysGluMetGlyArgGluLysCySHsgIntYrTTPProAla 316
 QY 1371 GAGGCTCTGCTGCTACCAAGTACTTTGTTTACCCGATGGCTGAGTACAAATGCC 1430
 Db GlutArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGlnTyrAsnMetPro 336
 QY 1431 CAGTATATCTGCGCTGAGTTCAAGGTACCGGATGCCGGATGGCGAGTCAAGGACA 1487
 Db GlnTyrIleLeuArgLysGluPheValThrAspAlaArgAspGlyGlnSerArgThr 355
 RESULT 14
 ID Q91BA2 PRELIMINARY; PRT; 468 AA.
 AC Q91BA2;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE RYPR2AB protein (Fragment).
 GN RYPR2AB.
 OS Potamotrygon motoro (South American freshwater stingray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squalae; Hypnosquales; Pristionotae; Batoidae;
 OC Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.
 OX NCBI_TaxID=86373;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20219325; PubMed=10754074;
 RA Ono-Koyanagi K., Suga H., Kato K., Miyata T.;
 RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
 RT divergence of tissue-specific isoform genes in the early evolution of
 RT vertebrates.";
 RL J. Mol. Evol. 50:302-311(2000).
 DR EMBL; AB03584; BAA35191.1; -.
 DR HSP; P18052; LYFO.
 DR GO; GO:0016787; P:hydrolase activity; IEA.
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; TYR_PP.
 DR Pfam; PF00102; Y_PTPase.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00194; PTPC; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_2; 2.
 KM Hydrolase.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 468 AA; 53865 MW; 8B1CAB0E8E969284 CRC64;
 Alignment Scores:
 Pred. No.: 8.16e-51 Length: 468
 Score: 59.00 Matches: 59
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.18% Indels: 0
 DB: 13 Gaps: 0
 US-09-719-272-1 (1-3467) x Q91BA2 (1-468)
 QY 1311 GTCATGCTGACCAAGCTTCGGAGATGGCGAGGAGAAATGCCACAGTACTGGCCAGCA 1370
 Db ValmetLeuthrLysLeuArgLysGluMetGlyArgGluLysCySHsgIntYrTTPProAla 316
 QY 1371 GAGGCTCTGCTGCTACCAAGTACTTTGTTTACCCGATGGCTGAGTACAAATGCC 1430
 Db GlutArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGlnTyrAsnMetPro 336
 QY 1431 CAGTATATCTGCGCTGAGTTCAAGGTACCGGATGCCGGATGGCGAGTCAAGGACA 1487

Db 337 GlnTyrlleuArgGluPheIysValThrAspAlaArgAspGlyGlnSerArgThr 355

RESULT 15

Q91BA0 PRELIMINARY; PRT; 468 AA.

AC Q91BA0; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, last annotation update)
DE RYTPR2AC protein (Fragment).
GN RYTPR2AC
OS Potamotrygon motoro (South American freshwater stingray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hypnosqualia; Pristiogaster; Batoida;
OC Myliobatiformes; Myliobatoidae; Potamotrygonidae; Potamotrygon.
OX NCBI_TaxID=86373;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20219325; PubMed=10754074;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;
RT divergence of tissue-specific isoform genes in the early evolution of
RT vertebrates.";
RT J. Mol. Evol. 50:302-311(2000).
DR EMBL; AB033586; BAA95193.1; -.
DR HSSP; P18052; 1XPO.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR00242; TYR_PP.
DR Pfam; PF0102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTPPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00393; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolyase.
KW NON TER
FT
SQ SEQUENCE 468 AA; 53976 MW; 76C975D92D437A86 CRC64;

Alignment Scores:

Pred. No.:	8.16e-51	Length:	468
Score:	59.00	Matches:	59
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.18%	Indels:	0
DB:	13	Gaps:	0

US-09-719-272-1 (1-3467) x Q91BA0 (1-468)

QY	1311	GTCAATGCTGACCAAGCTTGGAGATGGGACAGAGAAATGCCACCACTGAGCCACGA	1370
Db	297	ValMetLeuThrIleuArgGluMetGlyArgGluIysCysHISGlnTyrTrpProAla	316
QY	1371	GAGCGCTGCTGCTGCTACCAAGTACTTTGTTGACCCGATGGCTGAGTACCAATGCC	1430
Db	317	GluArgSerAlaArgTyrGlnTyrPheValValAspProMetCalaGlnTyrAsnMetPro	336
QY	1431	CAGTATATCTCGGTGAGTTCAAGTCAAGATGCCCGGATGGCAGTCAAGACACA	1487
Db	337	GlnTyrIleLeuArgGluPheIysValThrAspAlaArgAspGlyGlnSerArgThr	355

Search completed: March 9, 2004, 09:10:14
Job time : 207 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 9, 2004, 08:56:28 ; Search time 55 Seconds
(without alignments)
12127.126 Million cell updates/sec

Title: US-09-719-272-1

Perfect score: 1138
Sequence: 1 gatccgacgaagactcc.....atttgataatcagattctt 3467

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283366 seqs, 96191526 residues

Word size: 1

Total number of hits satisfying chosen parameters: 565818

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p model -DEV=xlp
-Q=/cgn2/USPRO.spool/p/US09719272/runat.09032004.085230.7466/app.query.fasta.1.3655
-DB=PIR_78 -QFMT=fastan -SUFFIX=xlp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdd -LIST=45
-DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco
-NORExt -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09719272.QCGN.1.1.87@runat.09032004.085230.7466 -NCPU=6 -ICPU=3
-NO MMAP -LARGESUBSTRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -Fgapop=6
-Fgapext=7 -YGAPOP=60 -YGAPEXT=60 -DELop=6 -DELExt=7

Database :

1: PIR_78:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	607	53.3	1897 1	TPHUK
2	259	22.8	1290 2	A56493
3	254	22.3	1898 2	S46216
4	254	22.0	582 2	A57068
5	108	9.5	108 2	S40292
6	59	5.2	398 2	I56540
7	59	5.2	1499 2	I50212
8	59	5.2	1501 2	I58148
9	59	5.2	1863 2	S46217
10	59	5.2	1807 2	S50893
11	59	5.2	1912 2	A56178
12	54	4.7	1691 1	C54689
13	54	4.7	1894 2	C54689
14	46	4.0	1231 2	S53089

15	40	3.5	1437 2	T31093	probable protein-t
16	40	3.5	1496 1	A48758	protein-tyrosine-p
17	34	3.0	2029 1	TPPFLK	protein-tyrosine-p
18	25	2.2	2051 2	T30938	receptor tyrosine
19	23	2.0	1262 1	B48758	protein-tyrosine-p
20	14	1.2	2302 2	T14328	protein-tyrosine-p
21	13	1.1	88 2	A44929	protein-tyrosine-p
22	13	1.1	106 2	S40282	protein-tyrosine-p
23	12	1.1	198 2	T27722	hypothetical prote
24	12	1.1	256 2	A40169	protein-tyrosine-p
25	12	1.1	483 2	T25992	hypothetical prote
26	12	1.1	521 1	A44267	protein-tyrosine-p
27	12	1.1	593 2	S17671	protein-tyrosine-p
28	12	1.1	689 2	JC6132	protein-tyrosine-p
29	12	1.1	700 1	S12053	protein-tyrosine-p
30	12	1.1	796 1	JC1285	protein-tyrosine-p
31	12	1.1	802 1	A36065	protein-tyrosine-p
32	12	1.1	829 1	A47373	protein-tyrosine-p
33	12	1.1	1174 2	I38140	protein-tyrosine-p
34	12	1.1	1175 2	S51005	protein-tyrosine-p
35	12	1.1	1176 2	JC4155	protein-tyrosine-p
36	12	1.1	1187 1	JC4155	protein-tyrosine-p
37	12	1.1	1189 1	JC2366	protein-tyrosine-p
38	12	1.1	1200 2	T43148	probable protein-t
39	12	1.1	1237 2	A54080	protein-tyrosine-p
40	12	1.1	1273 1	TPRTEL	leukocyte common a
41	12	1.1	1291 1	A28334	protein-tyrosine-p
42	12	1.1	1301 1	A41622	protein-tyrosine-p
43	12	1.1	1304 1	A46546	leukocyte common a
44	12	1.1	1422 2	T42636	protein-tyrosine-p
45	12	1.1	1440 2	JC6312	protein-tyrosine-p

ALIGNMENTS

RESULT 1
TPHUK
leukocyte antigen-related protein precursor - human
N/Alternate names: leukocyte common antigen homolog
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text change 22-Jun-1999
C/Accession: S03841, J01051
R/Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.
J. Exp. Med. 168, 1523-1530, 1988
A/Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region
A/Reference number: J01051, MIM:8903578, PMID:2972792
A/Residues: 1-1897 <SNP>
A/Molecule type: mRNA
A/Status: nucleic acid sequence not shown
A/Accession: S03841
C/Genetics:
A/Gene: GDB:PTRF, LAR
A/Cross-references: GDB:120138, OMIM:179590
A/Map position: lp34-1p34
C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology
C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
F/1-16/Domain: signal sequence #status: predicted <SIG>
F/17-1897/Product: leukocyte antigen-related protein #status: predicted <EXT>
F/17-1250/Domain: extracellular #status: predicted <EXT>
F/139-199/Domain: immunoglobulin homology <IMM>
F/236-290/Domain: immunoglobulin homology <IMM2>
F/303-390/Domain: fibronectin type III repeat homology <FN3A>
F/403-489/Domain: fibronectin type III repeat homology <FN3B>
F/501-583/Domain: fibronectin type III repeat homology <FN3C>
F/596-685/Domain: fibronectin type III repeat homology <FN3D>
F/698-798/Domain: fibronectin type III repeat homology <FN3E>
F/810-893/Domain: fibronectin type III repeat homology <FN3F>
F/905-989/Domain: fibronectin type III repeat homology <FN3G>
F/1001-1078/Domain: fibronectin type III repeat homology <FN3H>

F:1251-1274/Domain: transmembrane #status predicted <TM>
 F:1275-1897/Domain: intracellular #status predicted <INT>
 F:1285-1897/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:1365-1886/Domain: protein-tyrosine-phosphatase homology <PTP1>
 F:1654-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>
 F:144-97/146-197/243-288/Disulfide bonds: #status predicted
 F:107/240/288/711/956/Binding site: carbonyl (Aan) (covalent) #status predicted
 F:1538/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1544/Binding site: substrate phosphate (Arg) #status predicted
 F:1826/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1835/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:

Pred. No.:	Length:	Score:	Matches:	Conservative:	Mismatches:	Best Local Similarity:	Query Match:
0	1897	607.00	607	100.00%	0	100.00%	1
100.00%					0		
53.34%					0		
					0		

US-09-719-272-1 (1-3467) x TDHULK (1-1897)

```

QY 6 GGAAGTAAAGAGCTCCCTGGTGGCCCACTCTCTGACCCCTGTGAGATGGAGGCTCAAC 65
Db 1291 GYLLEULYASPSERLEUENLAHLSERSEAPROVALGLMECHARGLEUASN 1310
QY 66 TACCAAGACCCAGGATAGCGAGACCAACCCCAATCCCATCCAGCAAGCTGGCGGACAAAC 125
Db 1311 TYRGLNTHPRGILYMERHARGASPHISPROFOLLETHASPLEUHLAASPHEN 1330
QY 126 ATGAGACGCTCAAAACCAACGATGGCTCAAGTCTCCAGAGATGAGATGACATGAC 185
Db 1331 TLEGLIARGLEUYSALASNAHPGLYLEULYSPHESERGLNGLINUTYRGLISERLLEASP 1350
QY 186 CCGTGAACAGAGTTCAGTGGAGAAATTCAACTGAGAGTGAACAAGCCCAAGAACCCGC 245
Db 1351 PROGLYGLNGLINHERITRPGILUANSERASLEUGLUVALASMLYPROLYSASNAARG 1370
QY 246 TATGCGAATGTCAATGCCCTTACGACCACTCTCGAGTATACCTTACCTTACGATGGCGCTC 305
Db 1371 TYRALASNAVALLEALATYRAPHLSERARGVALILLEUNTHSERILLEASPLLYVAL 1390
QY 306 CCGGAGATGACTACATCAATGACCACTACATGATGAGTACCGCAAGCAAGATGGCTTAC 365
Db 1391 PROGLYSERASPHYRILLEASNAALASNAHYRILLEASPLLYTYRARGYGLINASNAALATYR 1410
QY 366 ATGCGCAACGAGGCGCCCTGCGGAGACCATGGCGATTTCTGAGGAATGGTGGGGA 425
Db 1411 LLEALATHRGLNGLYPROLEUPROGLUTHTMETGLYASPPHETTPARGMETVALITRPGILU 1430
QY 426 CAGGCGACGGGCACTGTGATCATGATGACAGGCTGGAGAGAAAGTCCCGGTAATAATGT 485
Db 1431 GLNHRGTHRALATHRALVALMETMETTHARGLEUGLULYSESRARGVALYSCYS 1450
QY 486 GATCAGTACTGGCCAGCCGCTGGGACCGAGACCTGTGGCTTATTCAGGTGACCTGTTTG 545
Db 1451 ASPGLNITRITRPROALAARGGLYTHRGILUTHRCYGLIYLEULLEGILVALTHIRLEUEN 1470
QY 546 GACACAGTGAAGCTGGGCAATACACATGTCGACCTGGACATCCCAAGATGGCTCC 605
Db 1471 ASPHRYVALGLULLEUALATHRYTRHVALARGTHPHEALALEUHLISYSSERGLYSER 1490
QY 606 AGTGAGAGCGTGAGCTGCGTCAAGTTTCAGTTCAATGGCTGGCCAGACCAATGAGTTCTCT 665
Db 1491 SERGLINYSARGILULEARGLINPHEGLINPHEMETLATRIPROASPHISGLYVALIPRO 1510
QY 666 GAGTAAACCACTCCCACTCGGCTTCTCTGACAGGGTCAAGGCTGGCAACCCCTAGAC 725
Db 1511 GLINUTRPROINPROILLEUALAPHEUALAPHEULARGVALYLSALACYSANPROLEUASP 1530
QY 726 GCAGGGCCCATGTGTGACATGACGCGGCGCTGGGCGGCAACGGCTGCTTCATGCTG 785
Db 1531 ALAAGLYPROMETVALVALHASCYSERLALGLYVALGLYARGTHRGILYCSPHLEILEVAL 1550

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QY 786 ATGATGACATGTTGAGAGCGATGAGACGAGAGAGCGGTGACATCTATGACCACTG 845
Db 1551 LLEASPHALMETLEUGLULARGMETYRSHISGLINUTYRTHRALASPLILETYRGLYHLEVAL 1570
QY 846 ACCGTGATCCGATCACAGAGAACTACATGTGTGACAGCGAGACCACTAGTGTTCATC 905
Db 1571 THRCYMETARGSERGLINARGASNAHYRMETVALGLNTHRGILUASPLITRYVALPHEILE 1590
QY 906 CATGAGCGCTGTGGAGGCTGCCAGTGGCGGCCACAGAGGTGCTGCCCGCAACCTG 965
Db 1591 HIEGLIUALLEUGLULALATHRCYSGILYHSTHNGILVALPROALARGASNALEU 1610
QY 966 TATGCCCAATCCAGAGAGCTGGGCCAAGTCTCCAGGGGAGAGTGTGACCCGCTGAG 1025
Db 1611 TYRALAHLEILEGLINYSLEUGLILYGLINVALIPROPROGLYGLINSEVALTHRALMETGLU 1630
QY 1026 CTCGAGTTCAAGTTGTGGCGCTGCGTCCAGAGGCCACACAGTCCGCTTACAGCCCAAC 1085
Db 1631 LEUGLIPHEYLEUENLAASERISERLYSALAHLETHSRARGPHEILESERLALASN 1650
QY 1086 CTGCGCTGCAACAAGTTCAAGAACCGGCTGTGAACTATGATCCCTTACGAATTGACCGGT 1145
Db 1651 LEUPROCYASNAHYSPHELYSASNAARGLEUVALASMLLEMETPROLYTGLINUTHRARG 1670
QY 1146 GTGTGCTGAGGCCCATCCGCTGTGAGAGGCGCTGACTATACATGATGACGCTTCTG 1205
Db 1671 VALCYSLIENGLINPROILLEARGILYVALGLINGLYSESRPHYRILLEASNALESERPHELEU 1690
QY 1206 GATGTTATAGACAGAGAGGCTTACATGCTTACACAGGGGCTTGGCAGAGAGACCC 1265
Db 1691 ASPLGLYTYRARGINGLINYSALATYRILLEATHRGLNGLYPROLEUHLAASPLIESTHR 1710
QY 1266 GAGGACTTCTGGGCGCATGCTTARGGAGCAATTCACATCATGCTGATGCTGAGCAAG 1325
Db 1711 GLUASPHETTPARGMETLEUTRPGILUHLASNAESTHRIILEVALMETLEUNTRYLS 1730
QY 1326 CTTGCGAGATGAGGCGAGGAGAAATGCCACAGTACTGGCCAGAGAGCGCTGCTGCTGC 1385
Db 1731 LEUARGILUMETGLYARGILULYSCYSHISGLINTYRTPROALGLUARGSERLALARG 1750
QY 1386 TACCAAGTCTTGTGTTGACCCGATGAGCTGAGTACAAATGCCCAAGTATACCTGGCT 1445
Db 1751 TYRGLINTRYRHEVALVALASPPROMETALAGLUTYRASMETPROGLINTYRILLEUENARG 1770
QY 1446 GAGTTCAAGGTCAACGATGCCCGGATGGGCACTGCAAGCAATCCGCAATTCCAGTTC 1505
Db 1771 GLUPHELYVALTHIRASPHALARGASPLYGINSERARGTHRIILEARGLINPHEGLINPHE 1790
QY 1506 ACAGACTGGCCAGAGCGGCGTGGCCCAAGACAGGCGAGGAGATTTCATTGATTCACCGGG 1565
Db 1791 THRASPTRPROGLINGLINLYVALIPROLYSTHNGILYGLINGLYPHEILEASPHLEILEGLY 1810
QY 1566 CAGGTGCAATAGACCAAGAGAGAGATTGACAGAGTGGGCTTACAGGTGCACTGCACT 1625
Db 1811 GLINVALHISYESTHRYLSGLINGLINPHEGLYGLINASPLIYPROLLETHRVALHISYSSER 1830
QY 1626 GCTGGCGTGGCGGCGAGGCTTTCATCATCTGTGACATGCTCTGAGGCCCAATGCCG 1685
Db 1831 ALAAGLYVALGLYARGTHNGILYVALPHEILETHIRLEUSERLLEVALLEUGLUARGMETARG 1850
QY 1686 TATAGAGGCGGTGCGACATGTTTCAGACCGTGAAGACCTGTGATACAGCTGCTGCC 1745
Db 1851 TYRGLINGLYVALVALASPMETPHEGLINTHVALYSTRLEUARGTHRGILINARGPROALA 1870
QY 1746 ATGTGACAGACAGAGACCAAGTATCACTGTGTCTTACCTGTGGCGCTTGGAGTACCTGGCG 1805
Db 1871 METVALGLINTRGILUASPLIGLINTYRGLINLEUCYERYTARGILALALEUGLUTYRLEUGLY 1890
QY 1806 AGCTTGAACCATGATGCAAG 1826
Db 1891 SERPHEASPHISLYRALATHR 1897

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QY 1317 CTGACCAAGCTTGGGAGATGGGAGGAAATGCCACCACTGACGAGGAGGAGC 1376
 DB 413 LeuThrIysLeuArgIleMetCGLyArgGluIuIscYshIsgIuIyrrTPProAlaGluArg 432
 QY 1377 TCTGCTCCGCTACCAAGTACTTGTGTTGTGACCCGATGGCTGAGTAAACATGCCAGTAT 1436
 DB 433 SerIlaArgIyrgIuIyPheValValAspProMetAlaGluIyrrAanMetProGIntyr 452
 QY 1437 ATCTGCTGAGTTCAGAGTCAAGGATGCCCGGATGGGCGATGGAAGACATCCGCGAG 1496
 DB 453 IleLeuArgGluIuIyValThrAspAlaArgAspGlyIuIyIserArgThrIleArgGln 472
 QY 1497 TTCAGTTCACAGACTGGCCAGAGAGGCGGCTGCCACAGAGCGGAGGATTCATTGAC 1556
 DB 473 PheGlnPheThrAspTrpProGluGlnIyValProIystrIuIyGluIyGluPheIleAsp 492
 QY 1557 TTCATGCGGACAGTGCATTAAGACCAAGAGAGCTTTGACACGATGGGCTTATCAAGGTG 1616
 DB 493 PheIleGlyGlnValIleHisIyThrIyIsgIuIyGlnPheGlyIuIyAspGlyProIleThrVal 512
 QY 1617 CACTGACAGTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1676
 DB 513 HisCySerIlaGlyValGlyArgThrIyValPheIleThrIleuSerIleValIleuGln 532
 QY 1677 CGCATGCGCTATGAGGCGGCGTGTGACATGTTTCAGACCGGTGAAGACCTTCGTTACAG 1736
 DB 533 ArgMetArgIyrgIuIyValValAspMetPheGlnThrValIystrIleuArgThrGln 552
 QY 1737 CGTCTGCGCATGTCGACACAGAGGACAGATTCAGCTGCTACCGGCGGCGGCGGCGGCGG 1796
 DB 553 ArgProIaMetValGlnThrIuIyAspGlnIyGlnIleuCyIyrrArgAlaIleuGln 572
 QY 1797 TACCTCGGACGCTTGACCACTATGCAAGC 1826
 DB 573 TyrLeuGlySerPheAspIleThrValThr 582
 RESULT 5
 S40292 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type f - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Mar-1994 #sequence_revision 15-Mar-1996 #text_change 23-Mar-2001
 C:Accession: S40292
 R:Henricks, W.; Brügman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
 Submitted to the EMBL Data Library, June 1993
 A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
 A:Reference number: S40292
 A:Accession: S40292
 A:Status: preliminary
 A:Stature: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-108 <EMBL>
 A:Cross-references: EMBL:223061, NID:g438159, PIDN:CA80596.1, PID:g438160
 C:Superfamily: Leukocyte antigen-related protein, fibronectin type III repeat homology;
 C:Keywords: glycoprotein; phosphoric monoester hydrolase; transmembrane protein; tyrosin
 F.1-108/Domain: leukocyte common antigen cytosolic domain homology (fragment) <LAC>
 Alignment Scores:
 Pred. No.: 9 54e-85 Length: 108
 Score: 108.00 Matches: 108
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 9.49% Indels: 0
 DB: 2 Gaps: 0
 US-09-719-272-1 (1-3467) x S40292 (1-108)
 QY 1293 CACAATTCACCACTCATCTGCTGATGACCAAGCTTGGGAGATGGGAGGAGAAATGC 1352
 DB 1 HisAsnSerThrIleIleValMetLeuThrIyLeuArgIuIyMetIyArgIuIyScys 20
 QY 1353 CACCACTGAGGAG 1412

DB 21 HisGlnIyrrTPProAlaGluArgSerIlaArgIyrgIuIyPheValValAspProMet 40
 QY 1413 GCTGAGTACCAATGCCCAAGATATCTGCGTGAAGTCAAGTCAAGATGCCCGGAT 1472
 DB 41 AlaGluIyrrAspMetProGIntyrIleuArgIuIyPheValThrAspAlaArgAsp 60
 QY 1473 GGGCAATCAAGACCAATCCGAGATTCATGACATGACATGACATGACATGACATGACATG 1532
 DB 61 GlyIuIySerArgThrIleArgIuIyPheGlnPheThrAspTrpProGluGlnIyValPro 80
 QY 1533 AAGACAGGAGGAGGATTCATGATTCATGCGGAGGTGATTAAGACCAAGAGAGATT 1592
 DB 81 LysThrGlyIuIyGlnPheIleAspPheIleGlyGlnValIleHisIyThrIyLeuGlnIle 100
 QY 1593 GGCACAGATGGGCTTATCAAGGTG 1616
 DB 101 GlyIuIyAspGlyProIleThrVal 108
 RESULT 6
 I56540 protein-tyrosine-phosphatase (EC 3.1.3.48) ctp1 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
 C:Accession: I56540
 R:Sahn, M.; Hockfield, S.
 J. Neurosci. 13, 4968-4978, 1993
 A:Title: Protein tyrosine phosphatases expressed in the developing rat brain.
 A:Reference number: I56540; MIMD:94045925; PMID:8229209
 A:Accession: I56540
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-398 <RES>
 A:Cross-references: EMBL:U03273, NID:g414996, PIDN:AAC52124.1, PID:g414997
 C:Genetic:
 A:Gene: ctp1
 C:Superfamily: Leukocyte antigen-related protein, fibronectin type III repeat homolo
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosph
 F.1-157/Domain: protein-tyrosine-phosphatase homology (fragment) <PTP>
 F.225-398/Domain: protein-tyrosine-phosphatase homology (fragment) <PTP>
 F.109/Active site: Cys (phosphocysteine intermediate) #status predicted
 F.115/Binding site: substrate phosphate (Arg) #status predicted
 Alignment Scores:
 Pred. No.: 2 02e-42 Length: 398
 Score: 59.00 Matches: 59
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.18% Indels: 0
 DB: 2 Gaps: 0
 US-09-719-272-1 (1-3467) x I56540 (1-398)
 QY 1311 GTCATGTGACCAAGCTTGGGAGATGGGAGGAGAAATGCCACCACTGACGAGGAGC 1370
 DB 297 ValMetLeuThrIyLeuArgIuIyMetCGLyArgGluIuIyCyHisGlnIyrrTPProAla 316
 QY 1371 GAGCGCTCTGCTGCTACCAAGTACTTGTGTTGTGACCCGATGGCTGAGTAAACATGCC 1430
 DB 317 GluArgSerIlaArgIyrgIuIyPheValValAspProMetAlaGluIyrrAanMetPro 336
 QY 1431 CAGTATTCCTGCTGATGATTCAGAGTCAAGGATGCCCGGATGGGCGATGCAAGAGACA 1487
 DB 337 GlnIyrrIleuArgIuIyPheValThrAspAlaArgAspGlyIuIyIserArgThr 355
 RESULT 7
 I50212 protein-tyrosine-phosphatase (EC 3.1.3.48) - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
 C:Accession: I50212
 R:Stoker, A.W.
 Mech. Dev. 46, 201-217, 1994

Alignment Scores:	
Pred. No.:	1,496-42
Score:	59.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	5,188
DB:	2
	Gaps:
US-09-719-272-1 (1-3467) x IS0212 (1-1499)	1499
	Matches:
	59
	Conservative:
	0
	Mismatches:
	0
	Indels:
	0
	Gaps:
	0

US-09-719-272-1 (1-3467) X I50212 (1-1499)

Qy	1311	GTGATGCTGACCAACCTTCGGGAGATGGGAGGAGAAATGGCAACCAATACGGCACACA	13170
Db	1329	ValMetLeuThrIlyLeuArgGluMetGlyArgGlnIlyScyShhGlnIlyTyrTrpProIa	13488
Qy	1371	GAGGCGCTTCGCGGTATCCAGATCACTTGTGTGTACCCGAGTGGCTAGTACAACATGGCC	14303
Db	1389	GluArgSerAlaIahGlyIyGlnIyPheValValIahProMetAlaGlnIlyIAsMetPro	13666
Qy	1431	CAGTATATCTCGCGTGAAGTTCAGAGTCACGATCCCGGAGTGGCGAATCAAGACACA	1487
Db	1369	GlnIlyTyrIleLeuArgGlnPheIyValThrAspAlaIahGAspGlyGlnIserGlyThr	1387

RESULT 8
I58148

protein-tyrosine-phosphatase (EC 3.1.3.48) 2B, splice form IAR - rat
N:Alternate names: leukocyte common antigen-related phosphatase
C:Species: Rattus norvegicus (Norway rat)

C;Date: 26-Jul-1996 #sequence 26-Jul-1996 #text_change 20-Jun-2000

C/Accession: 158148; S46218
R;Walton, K.M.; Martell, K.U.; Kwak, S.P.; Dixon, J.E.; Largent, B.L

Neuron 11, 387-400, 1993
A; Title: A novel receptor-type protein tyrosine phosphatase is expressed during neurogen

A;Reference number: 158148; MUID:93357030; PMID:8352946
A;Accession: 158148

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A/Residues: 1-1501 <WAL>
A/Cross-references: GB:L19933 NID:Q310242 PIDN:AAA42309.1 PID:Q310243

A;Note: in Genbank entry RATTYRPHOS, release 113.0, the source is design
P.Zhang W.P. Hashimoto N. Ahmad E. Ding W. Goldstein B.J.

Wang, J. C. 1994. Molecular cloning and expression of a myofibrillar-like protein-tyrosine-phosphatase. *J. Biol. Chem.* 269: 13947-13952.

A/Reference number: S46216; MUID:94347119; PMID:8068021

A;Accession: 546216
A;Status: translation not shown

A;Molecule type: mRNA
A;Residues: 1-1501 <ZHA>

A; Cross-references: EMBL:L12329; NID:g294573; PIDN:AAC37657.1; PID:g294574
C; Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyros

[illegible]

US-09-719-272-1 (1-3467) x I58148 (1-1501

QY	1311	GTCTGTGTGACCAAGCTCTGGAGAGATTTGGGACGGAGAAATGCCACCAAGTCTGGCCACGACA	1379
Db	1330	ValMetLeuThrIyrIseLeuAgiGluMetGIYArgGluIyrScySHsGlnIyrTrpProAla	1349
QY	1371	GAGGCGCTGTGCTGCCTACCAAGTACTTTGTGTGTGACCCGATGTGGCTAGATCAACATCACC	1430
Db	1350	GluArgSerHisIaArgIyrGlnIyrPheValValAspProMetIaGlnIyrAspMetPro	1369
QY	1431	CAGATATTCCTGGGTGAGTTCAAGGTACGAGATGCCGGATGGGACGTCGAACAGACA	1487
Db	1370	GlnIyrIleuLeuAgiGluPheIyrValIthrAspIaIArgAspGlyGlnIserArgIthr	1388

RESULT 9
S46217

N/Alternate names: leukocyte common antigen-related phosphatase
C/Species: Rattus norvegicus (Norway rat)

C:\Date: 07-May-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C:\Accession: S46217; S51174; A49104

R.; Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J. *Biochem. J.* 302, 39-47, 1994

A/Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine
A/Reference number: S46216: MUID:34347119: PMID:8068021

A/Accession: S46217
A/Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A; Cross-references: EMBL:L11587

R/Goldstein, B.U.
submitted to the EMBL Data Library, February 1993

A;Reference number: S51174
A;Accession: S51174

A;Molecule type: mRNA
A;Residues: 1-1788, 'G', 1790-1863 <GOL>

A./Cross-references: EMBL:U11587; NID:g205134; PIDN:AAC37656.1; PID:g205135
R.Yan, H.: Grossman, A.: Wang, H.: D'Eustachio, P.: Mossie, K.: Musacchio, J.M.: Si-

J. Biol. Chem. 268, 24880-24886, 1993

A;Reference number: A49104; MUID: 94043351; PMID: 82270504
A;Accession: A49104

A; Status: preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid

A/Residues: 1-596, 'R', 598-603, 'I', 967-1788, 'G', 1790-1863 <YAN>

A/Note: Sequence extracted from NCBI backbone (NCBI:139669)

C/superficially: leukocyte antigen-related protein; idiomecln type III repeat homology

Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphatase; signal sequence #status predicted <SIG> F;1-26/Domain:

F;27-1863/Product: protein-tyrosine-phosphatase
F;149-209/Domain: immunoglobulin homology <IMM1>

F.246-300/Domain: immunoglobulin homology <IMM2>
 F.318-400/Domain: fibronectin type III repeat homology <FN3A>
 F.413-499/Domain: fibronectin type III repeat homology <FN3B>
 F.511-592/Domain: fibronectin type III repeat homology <FN3C>
 F.1244-1863/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F.1331-1552/Domain: protein-tyrosine phosphatase homology <PTP1>
 F.1504/Active site: Cys (phosphocysteine intermediate) #status predicted
 F.1510/Binding site: substrate phosphate (Arg) #status predicted
 F.1795/Active site: Cys (phosphocysteine intermediate) #status predicted
 F.1801/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:

Pred. No.:	1-42e-42	Length:	1863
Score:	59.00	Matches:	59
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.18%	Indels:	0
DB:	2	Gaps:	0

US-09-719-272-1 (1-3467) x S46217 (1-1863)

QY 1311 GTCATGCTGACCAAGCTTGGAGATGGCGAGGAAATGCCACGACTGCGCCGCA 1370
 Db 1692 ValmetLeuThrLysLeuArgGluMetGlyArgGlnLysCysHisGlnTyrrProAla 1711
 QY 1371 GAGCGCTGCTCGGTACCAAGTCTTGTGTGACCCGAGTGGCTGAGTCAACATGCC 1430
 Db 1712 GUAAGSerAlaArgTyrrGlnTyrrPheValValaPpromeAlaGlnTyrrAsnMetPro 1731
 QY 1431 CAGTATATCTGCTGCTGAGTCAAGGTCCGAGTGGCGAGTGGCGAGTCAAGACA 1487
 Db 1732 GlnTyrrLeuArgGluPheValThrAspAlaArgAspGlyGlnSerArgThr 1750

RESULT 10

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type sigma precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
 A/Accession: S50893; S40281
 R/Wagner, J.; Boerboom, D.; Tremblay, M.L.
 Eur. J. Biochem. 226, 773-782, 1994
 A/Title: Molecular cloning and tissue-specific RNA processing of a murine receptor-type
 A/Reference number: S50893; MUID:95112841; PMID:7529177
 A/Accession: S50893
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-1907 <WAG>
 A/Cross-references: EMBL:X82288; NID:G587483; PIDN:CAA57732.1; PID:G587484
 R/Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
 submitted to the EMBL Data Library, June 1993
 A/Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
 A/Reference number: S40280
 A/Accession: S40281
 A/Molecule type: mRNA
 A/Residues: 1441-1501, 'E', 1503-1546 <HEN>
 A/Cross-references: EMBL:Z23050; NID:G438137; PIDN:CAA0585.1; PID:G438138
 C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
 C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane

F.149-209/Domain: immunoglobulin homology <IMM2>
 F.246-300/Domain: immunoglobulin homology <IMM2>
 F.413-506/Domain: fibronectin type III repeat homology <3PR>
 F.1288-1907/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F.1331-1552/Domain: protein-tyrosine phosphatase homology <PTP1>
 F.1504-1887/Domain: protein-tyrosine phosphatase homology <PTP2>
 F.1548/Active site: Cys (phosphocysteine intermediate) #status predicted
 F.1554/Binding site: substrate phosphate (Arg) #status predicted
 F.1833/Active site: Cys (phosphocysteine intermediate) #status predicted
 F.1845/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:	1-42e-42	Length:	1907
Pred. No.:	59.00	Matches:	59

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.18%	Indels:	0
DB:	2	Gaps:	0

US-09-719-272-1 (1-3467) x S50893 (1-1907)

QY 1311 GTCATGCTGACCAAGCTTGGAGATGGCGAGGAAATGCCACGACTGCGCCGCA 1370
 Db 1736 ValmetLeuThrLysLeuArgGluMetGlyArgGlnLysCysHisGlnTyrrProAla 1755
 QY 1371 GAGCGCTGCTCGGTACCAAGTCTTGTGTGACCCGAGTGGCTGAGTCAACATGCC 1430
 Db 1756 GUAAGSerAlaArgTyrrGlnTyrrPheValValaPpromeAlaGlnTyrrAsnMetPro 1775
 QY 1431 CAGTATATCTGCTGCTGAGTCAAGGTCCGAGTGGCGAGTGGCGAGTCAAGACA 1487
 Db 1776 GlnTyrrLeuArgGluPheValThrAspAlaArgAspGlyGlnSerArgThr 1794

RESULT 11

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - human
 N/Alternate names: protein-tyrosine-phosphatase BPTP-2
 C/Species: Homo sapiens (man)
 C/Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 21-Jan-2000
 A/Accession: A56178; S12052; B44929
 R/Pullid, R.; Krueger, N.X.; Serra-Pages, C.; Salto, H.; Streuli, M.
 J. Biol. Chem. 270, 6722-6728, 1995
 A/Title: Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta isoforms.
 A/Reference number: A56178; MUID:95204468; PMID:7896816
 A/Accession: A56178
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-1912 <PU>
 A/Cross-references: GB:IJ38929; NID:G755652; PIDN:AA41749.1; PID:G755653
 R/Krueger, N.X.; Streuli, M.; Salto, H.
 EMBO J. 9, 3241-3252, 1990
 A/Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatase
 A/Reference number: S12049; MUID:9106018; PMID:2170109
 A/Accession: S12052
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 390-1912 <RU>
 A/Cross-references: GB:X54133; NID:G35789; PIDN:CAA8068.1; PID:G35790
 A/Note: the sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 56
 R/Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Imai, K.;
 Cancer Res. 52, 7337-740, 1992
 A/Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.
 A/Reference number: A44929; MUID:92119637; PMID:1370651
 A/Accession: B44929
 A/Molecule type: mRNA
 A/Residues: 1756-1804, 'C', 1806-1845 <ADA>
 A/Cross-references: GB:S78086; NID:G243545; PIDN:AA821147.1; PID:G243546
 A/Experimental source: pre-B cell NALM-6
 A/Note: sequence extracted from NCBI backbone (NCBI:78086, NCBI:78087)
 A/Note: the authors did not report the entire codon for residue 90
 C/Genetics:
 A/Gene: GDB:PTPRD
 A/Cross-references: GDB:131384; OMIM:601598
 A/Map position: 9p24-9p24
 C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
 C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane

F.149-209/Domain: immunoglobulin homology <IMM2>
 F.246-300/Domain: immunoglobulin homology <IMM2>
 F.413-506/Domain: fibronectin type III repeat homology <3PR>
 F.1288-1907/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F.1331-1552/Domain: protein-tyrosine phosphatase homology <PTP1>
 F.1504-1887/Domain: protein-tyrosine phosphatase homology <PTP2>
 F.1548/Active site: Cys (phosphocysteine intermediate) #status predicted
 F.1554/Binding site: substrate phosphate (Arg) #status predicted
 F.1833/Active site: Cys (phosphocysteine intermediate) #status predicted
 F.1845/Binding site: substrate phosphate (Arg) #status predicted

SS3089
 protein-tyrosine-phosphatase (EC 3.1.3.48) AnLAR - African malaria mosquito (fragment)
 N/Alternate names: leukocyte antigen-related protein
 C/Species: Anopheles gambiae (African malaria mosquito)
 C/Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C/Accession: S53089
 R/Spiers, S.
 submitted to the EMBL Data Library, March 1995
 A/Description: Anlar-a transmembrane, receptor-like protein tyrosine phosphatase from th
 A/Reference number: S53089
 A/Accession: S53089
 A/Molecule type: DNA
 A/Residues: 1-1231 <SPI>
 A/Cross-references: EMBL:X85217; NID:G732549; PIDD:CAA59483.1; PIDD:G732550
 C/Genetics:
 A/Introns: 1026/3; 1070/3; 1209/3
 C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology/
 C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
 F/208-293/Domain: fibronectin type III repeat homology <3FR>
 F/618-1231/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F/988-1211/Domain: protein-tyrosine-phosphatase homology <PTP>
 F/872/Active site: Cys (phosphocysteine intermediate) #status predicted
 F/1163/Active site: Cys (phosphocysteine intermediate) #status predicted
 F/1169/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:

Pred. No.:	2,866-31	Length:	1231
Score:	46.00	Matches:	46
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	4.04%	Indels:	0
DB:	2	Gaps:	0

US-09-719-272-1 (1-3467) x S53089 (1-1231)

QY 1545 GGATTCATGACTTATCGGCGAGGATGATTAAGACAGAGAGATTGACAGATGG 1604
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 DB 1118 GlypHeIIeAspHeIIeGlyGlnValHIslyeThrlySGluGlnPheGlyGlnAspGly 1157
 |||||
 QY 1605 CCTATCAGGTCAGTGCAGTCTGCGCTGCGCCGACCGGGGTTCATCATCTTGAGC 1664
 |||||
 DB 1158 ProIleThrValHIsCysSerAlaGlyValGlyArgThrGlyValPheIleThrLeuSer 1177
 |||||
 QY 1665 ATCGTCTGGAGCGCATG 1682
 |||||
 DB 1178 ILeValIleuGluArgMet 1183
 |||||

RESULT 15

T31093

probable protein-tyrosine-phosphatase (EC 3.1.3.48) - medicinal leech

N/Alternate names: receptor tyrosine phosphatase

C/Species: Hirudo medicinalis (medicinal leech)

C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000

C/Accession: T31093

R/Gershon, T.R.; Baker, M.; Nitabach, M.; Wu, P.; Macagno, E.R.

submitted to the EMBL Data Library, December 1997

A/Description: Two receptor tyrosine phosphatases expressed by neurons and muscle cells

A/Reference number: Z20976

A/Accession: T31093

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1437 <GER>

A/Cross-references: EMBL:AF017084; NID:G2695656; PIDD:G2695657; PIDD:AB91461.1

C/Genetics:

A/Gene: LARI

C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology/
 C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane

Alignment Scores:

Pred. No.:	4,376-26	Length:	1437
Score:	40.00	Matches:	40

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.51%	Indels:	0
DB:	2	Gaps:	0

US-09-719-272-1 (1-3467) x T31093 (1-1437)

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 DB 1294 GluTyAsnMetProGlnIlyrIleuunrGluPheIyValThrAspAlaArgAspGly 1313
 |||||
 QY 1476 CAGTCAAGGACAAATCCGGAGTTCAGATTCAAGACTGACGAGAGAGAGGCGGCCAAG 1535
 |||||
 DB 1314 GlnSerArgThrIleArgGlnPheGlnPheThrAspTrpProGluGlnGlyValProIys 1333
 |||||

Search completed: March 9, 2004, 09:12:29
 Job time : 106 sec

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 9, 2004, 08:57:13 ; Search time 34 Seconds
(without alignments)

10528.661 Million cell updates/sec

Title: US-09-719-272-1

Sequence: 1138

Sequence: 1 gaccgcgaaggaagcacc.....atttgataatcagattctc 3467

Scoring table:

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Xgapop 60.0, Xgapext 60.0
Xgapop 6.0, Xgapext 7.0
Delop 6.0, Delext 7.0

Searched: 389414 seqs, 51625971 residues

Word size: 1

Total number of hits satisfying chosen parameters: 663654

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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-DB=Issued_Patents_AA -OPMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database:

Issued_Patents_AA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	289	25.4	289	1	US-08-036-210-13
2	289	25.4	289	1	US-08-049-609-13
3	289	25.4	289	4	US-09-361-096A-13
4	202	17.8	250	2	US-08-685-992-7
5	202	17.8	250	2	US-08-144-925-7
6	197	17.3	245	2	US-08-685-992-26
7	197	17.3	245	2	US-08-144-925-26
8	95	8.3	95	1	US-08-202-389-21
9	59	5.2	1501	1	US-08-447-464-3
10	59	5.2	1501	1	US-08-716-679-3
11	59	5.2	1911	1	US-08-348-068-5
12	59	5.2	1911	2	US-08-800-825A-5

13	59	5.2	1911	3	US-09-158-657-5	Sequence 5, Appl1
14	59	5.2	1911	5	PCT-US94-10166-5	Sequence 5, Appl1
15	47	4.1	95	1	US-08-202-389-22	Sequence 22, Appl1
16	31	2.7	95	1	US-08-202-389-23	Sequence 23, Appl1
17	14	1.2	14	2	US-08-480-190-241	Sequence 241, App
18	14	1.2	14	2	US-08-488-379-241	Sequence 241, App
19	14	1.2	14	4	US-08-475-399A-241	Sequence 241, App
20	14	1.2	14	4	US-08-475-399A-241	Sequence 241, App
21	14	1.2	14	5	PCT-US93-07545-241	Sequence 9, Appl1
22	14	1.2	176	2	US-08-036-210-15	Sequence 9, Appl1
23	14	1.2	176	2	US-08-449-609-9	Sequence 9, Appl1
24	14	1.2	289	4	US-09-361-096A-9	Sequence 47, Appl
25	14	1.2	322	4	US-08-036-210-11	Sequence 11, Appl
26	14	1.2	322	2	US-08-449-609-11	Sequence 11, Appl
27	14	1.2	322	4	US-09-361-096A-11	Sequence 11, Appl
28	14	1.2	401	4	US-09-361-096A-15	Sequence 15, Appl
29	14	1.2	402	2	US-08-449-609-15	Sequence 15, Appl
30	14	1.2	402	2	US-08-036-210-15	Sequence 22, Appl
31	14	1.2	898	1	US-08-036-210-12	Sequence 22, Appl
32	14	1.2	898	2	US-08-449-609-12	Sequence 22, Appl
33	14	1.2	898	4	US-09-361-096A-22	Sequence 22, Appl
34	12	1.1	235	4	US-08-015-985-5	Sequence 5, Appl1
35	12	1.1	235	4	US-09-280-597-5	Sequence 5, Appl1
36	12	1.1	236	4	US-08-015-985-6	Sequence 6, Appl1
37	12	1.1	236	4	US-09-280-597-6	Sequence 6, Appl1
38	12	1.1	242	1	US-08-015-985-7	Sequence 7, Appl1
39	12	1.1	242	4	US-09-280-597-7	Sequence 7, Appl1
40	12	1.1	248	1	US-08-015-985-9	Sequence 9, Appl1
41	12	1.1	248	4	US-09-848-294-10	Sequence 10, Appl1
42	12	1.1	248	4	US-09-280-597-9	Sequence 9, Appl1
43	12	1.1	253	2	US-08-685-992-10	Sequence 10, Appl1
44	12	1.1	253	2	US-08-685-992-11	Sequence 11, Appl1
45	12	1.1	253	2	US-09-144-925-10	Sequence 10, Appl1

ALIGNMENTS

RESULT 1
US-08-036-210-13
Sequence 13, Application US/08036210
Patent No. 5585233
GENERAL INFORMATION:
APPLICANT: Molier, Niels P.H.
APPLICANT: Molier, Karin B.
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
PHOSPHATASE
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,210
FILING DATE: 23-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET INFORMATION: 7683-025
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 289 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-036-210-13

Alignment Scores:

Pred. No.:	1,536-257	Length:	289
Score:	289.00	Matches:	289
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	25.40%	Indels:	0
DB:	1	Gaps:	0

US-09-719-272-1 (1-3467) x US-08-036-210-13 (1-289)

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DB 1 MetArgAspHisProProlleProIleThrAspLeuAlaAspAsnIleGluArgLeuLys 20
QY 141 GCCAAGCATGCTCTCAAGTTCTCCAGAGATATGATGATCCATGACCCCTGAGCAGCATTC 200
DB 21 AlaAsnAspGlyLeuLysPheSerGlnGluSerIleAspProGlyGlnGlnPhe 40
QY 201 ACGTGGAGATTTCAACCTGAGAGTGAACAAGCCCAAGAACCGCTATGCGAATGTCATC 260
DB 41 ThrTgPgluAsnSerAsnLeuGluValAsnLysProLysAsnArgTyrAlaAsnValIle 60
QY 261 GCGTCAGACCACTCTCGAATCTCTTACTTATCGATGGGTCCCGGAGAGTAC 320
DB 61 AlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyValProGlySerAspTyr 80
QY 321 ATCAATGCCAATCATCATGATGCTTACCGCAAGCAAGAAATGCTTATGCTGAGCGAG 380
DB 81 IleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGly 100
QY 381 CCCCTGCGGAGACCATGAGCGCATTTCTGAGAAATGCTGTGGAAACAGCGCAGCGCAT 440
DB 101 ProlLeuProGluThrMetGlyAspPheTyrPargMetValTyrGluGlnArgThrAlaThr 120
QY 441 GTGCTCATATGACACAGCGCTGGAGAGAGAGTCCCGGATTAATGATGATGATGAGCA 500
DB 121 ValValMetMetThrArgLeuGlnGluLysSerArgValLysCysAspGlnTyrTrpPro 140
QY 501 GCCCTGAGCACCGAGACCTGTGACCTTATTCAGGTGACCTGTTGAGCAAGTGAAGCTG 560
DB 141 AlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuAspThrValGluLeu 160
QY 561 GCCACATACCTGTGGGACCTTGGACCTCCCAAGAGTGGCTCCGAGAGAGGAGTGA 620
DB 161 AlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySerSerGluLysArgGlu 180
QY 621 CTGCGTCAGATTGATTCATGCTGCTGCGCAGACCATGAGATTCTTGAATCCCACTCC 680
DB 181 LeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGluTyrProThrPro 200
QY 681 ATCTGGCGCTTCTCAAGACGGGTCAAGGCTGCAACCCCTTAAGCCAGAGGCGCAATG 740
DB 201 IleLeuAlaPheLeuAlaArgValLysValaCysAsnProLeuAspAlaGlyProMetVal 220
QY 741 GTGACATGACCGGCGGCGTGGCGCGACCGGCTGCTTCATCGTGAATGATGCGCATGTTG 800
DB 221 ValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeu 240
QY 801 GAGCGATGAAGACAGAGAGAGCGGTGACATCTATGCGACATGACCTGAGCAGCATCA 860
DB 241 GluArgMetLysHisGluLysThrValAspIleTyrIleValIleThrCysMetArgSer 260
QY 861 CAGAGAACTCATGCTGAGACGAGACGAGACCATGATGCTTCAATCAATGAGGCGCTGCTG 920
DB 261 GlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIleHisGluAlaLeuLeu 280
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QY 921 GAGCTGCCACGTGGCGGCAACAGAG 947
DB 261 GluAlaAlaThrCysGlyHisThrGlu 289

RESULT 2

US-08-449-609-13

Application US/08449609

Sequence 13 5952212

Patent No 5952212

GENERAL INFORMATION:

APPLICANT: Moller, Niels P.H.

APPLICANT: Moller, Karin B.

TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/449,609

FILING DATE: 24-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/036,210

FILING DATE: 23-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Mierstock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7683-025

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 289 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: protein

Alignment Scores:

Pred. No.:	1,536-257	Length:	289
Score:	289.00	Matches:	289
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	25.40%	Indels:	0
DB:	2	Gaps:	0

US-09-719-272-1 (1-3467) x US-08-449-609-13 (1-289)

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QY 81 ATGGAGACCAACCCACCCATCCCATCAACGAGCGGAGCAACATCGAGCGCTCAAA 140
DB 1 MetArgAspHisProProlleProIleThrAspLeuAlaAspAsnIleGluArgLeuLys 20
QY 141 GCCAAGCATGCTCTCAAGTTCTCCAGAGATATGATGATCCATGACCCCTGAGCAGCATTC 200
DB 21 AlaAsnAspGlyLeuLysPheSerGlnGluSerIleAspProGlyGlnGlnPhe 40
QY 201 ACGTGGAGATTTCAACCTGAGAGTGAACAAGCCCAAGAACCGCTATGCGAATGTCATC 260
DB 41 ThrTgPgluAsnSerAsnLeuGluValAsnLysProLysAsnArgTyrAlaAsnValIle 60
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LENGTH: 250 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-144-925-7

Alignment Scores:

Pred. No.:	2,14e-177	Length:	250
Score:	202.00	Matches:	250
Percent Similarity:	97.66%	Conservative:	0
Best Local Similarity:	97.66%	Mismatches:	0
Query Match:	17.75%	Indels:	6
DB:	2	Gaps:	0

US-09-719-272-1 (1-3467) x US-09-144-925-7 (1-250)

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QY 255 GTCAATGCGCTACAGCACTCTGAGTATCTTACTCTATCGATGGCGTCCCGGAGAT 314
DB 21 ValIleAlaIleAspHisSerArgValIleLeuThrSerIleAspGlyValProGlySer 40
QY 315 GACTACATCAATGCCAATCATGATGCTACCGCAAGCAAGATGCTTACATCGCCAG 374
DB 41 AspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThr 60
QY 375 CAGGAGCCCGCTGCGGAGCAACCATGGGAGATTTCTGAGAAATGGTGGGAAACGCG 434
DB 61 GlnGlyProLeuProGlnThrMetGlyAspPheTrpArgMetValTrpGlnGlnThr 80
QY 435 GCCACTGTGTCATGATGACACGCGCTGAGAGAGAAATCCCGGTAATGTATCATGATAC 494
DB 81 AlaThrValValMetMetThrArgLeuGlnLysSerArgValLysCysAspGlnTyr 100
QY 495 TGGCAGCCCGCTGCGGAGCAACCATGGGAGATTTCTGAGAAATGGTGGGAAACGCG 554
DB 101 TrpProAlaArgGlyThrGlnThrCysGlnLeuIleGlnValThrLeuLeuAspThrVal 120
QY 555 GAGCTGGCCACATCACTGTGCGGACCTTGGCACTCCCAAGAGTGGCTCCAGTGAAG 614
DB 121 GluLeuAlaThrTyrThrVal-----PheAlaLeuHisLysSerGlySerGlnLys 138
QY 615 CGTAGCTGCTGCTGAGTTTCACTTCACTTGGCGGCAAGCAATGAGTTCCTGAGTACCA 674
DB 139 ArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGlnTyrPro 158
QY 675 ACTCCCATCTGCGCTTCTTACGACGCGGTCAAGGCTTCAACCCCTTGAAGCGAGGCC 734
DB 159 ThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAspAlaGlyPro 178
QY 735 ATGTGTGTGTCATGACAGCGCGGCGCTGGCGGCAACCGGCTGCTTCACTGATGATGCC 794
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QY 855 CGATCAACAGAGAACTTACATGCTGTCAGACGAGAGCAAGCAAGCAAGCAAGCAAGCAAG 914
DB 219 ArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIleHisGlnAla 238
QY 915 CTGTGTGAGGCTGCGGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 950
DB 239 LeuLeuGlnAlaAlaIleThrCysGlyHisThrGlnVal 250

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RESULT 6
 US-08-685-992-26
 ; Sequence 26, Application US/08685992
 ; Patent No. 5912138

GENERAL INFORMATION:
 APPLICANT: Tonks, Nicholas
 APPLICANT: Flint, Andrew J.
 TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 TITLE OF INVENTION: TYROSINE PHOSPHATASES
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESS: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 STREET: Two Millitia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FASTSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/685,992
 FILING DATE: 25-JUL-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCES/DOCKET NUMBER: CSHL96-03
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 781-861-6240
 TELEFAX: 781-861-9540
 TELEX:

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
 LENGTH: 245 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-685-992-26

Alignment Scores:
 Pred. No.: 8.64e-173 Length: 245
 Score: 197.00 Matches: 245
 Percent Similarity: 97.61% Conservative: 0
 Best Local Similarity: 97.61% Mismatches: 0
 Query Match: 17.31% Indels: 6
 DB: 2 Gaps: 0

US-09-719-272-1 (1-3467) x US-08-685-992-26 (1-245)

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QY 1122 ATATGCTCTTGAAGATTTGACCCGCTGTGCTGCAAGCCCATCGGAGTGGAGGCTCT 1181
DB 21 IleMetProTyrGlnLeuThrArgValCysLeuGlnProIleArgGlyValGlnLysSer 40
QY 1182 GACTACATCAATGCCAAGCTTCTGATGTTTATGACAGCAAGAGGCTTACATGACTTACA 1241
DB 41 AspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnGlnLysAlaTyrIleAlaThr 60
QY 1242 CAGGAGCCCTTGGCAAGAGCAACGAGCACTTGGCGGCAAGCAAGCAAGCAAGCAAGTCC 1301
DB 61 GlnGlyProLeuAlaGlnSerThrGluAspPheTrpArgMetLeuTrpGlnHisSer 80
QY 1302 ACCATCATGCTCATGCTGACCAAGCTTCGGAGATGGGAGAGAGAAATGCCACCAAGTAC 1361
DB 81 ThrIleIleValMetLeuThrLysLeuArgGlnMetGlyArgGlnLysCysHisGlnTyr 100
QY 1362 TGGCCAGAGAGGCGCTGCTGCTGCTACCAAGTACTTTGTGTGACCCGATGGCTAGATAC 1421

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Db 101 TTPProAlaGluHisSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyr 120
 QY 1422 AACATGCCCGCACTATATCTCGTGAAGTTCAAGTCCAGATGCCCGGATGGGAGTCA 1481
 Db 121 AsnMetProGlnTyrIleLeu-----PheLysValIleThrAspAlaArgAspGlyGlnSer 138
 QY 1482 AGGACAAATCCGGCAGTCCAGTTCAAGACTGGCCAGAGCAGGGCGTCCCAAGACAGGC 1541
 Db 139 ArgThrIleArgGlnPheGlnPheThrAspIleProGlnGlnGlnValProLysThrGly 158
 QY 1542 GAGGATTCATTGACTTCACTCCGCGAGTGCATTAAGACCAAGACGACTTTGACAGGAT 1601
 Db 159 GluGlyPheIleAspPheIleGlyGlnValHisLysThrLysGlnGlnPheGlyGlnAsp 178
 QY 1602 GGGCCTATACAGGTGACAGTGCAGTGCAGGCGGCGGCGGCGGAGTTCATCACTCTG 1661
 Db 179 GlyProIleThrValHisCysSerAlaGlyValGlyAspThrGlyValPheIleThrLeu 198
 QY 1662 AGCATGCTCCTGAGCGCATGCGCTATGAAGGCGTGTGACATGTTTCAAGCCGTGAAG 1721
 Db 199 SerIleValLeuGlnArgMetArgTyrGlnGlyValValAspMetPheGlnThrValLys 218
 QY 1722 ACCCTGCTTACAGAGGCTCTGCTGCAAGTGTGACAGACAGAGACCAAGTACAGTGTAC 1781
 Db 219 ThrLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGlnTyrGlnLeuGlyTyr 238
 QY 1782 CGTGGGCGCTGGAGTACCTC 1802
 Db 239 ArgAlaAlaLeuGlnTyrLeu 245
 RESULT 7
 US-09-144-925-26
 ; Sequence 26, Application US/09144925
 ; Patent No. 5951979
 ; GENERAL INFORMATION:
 ; APPLICANT: Tocks, Nicholas
 ; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 ; TITLE OF INVENTION: TYROSINE PHOSPHATASES
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P. C.
 ; STREET: Two Milcila Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02421-4799
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: FastSeq for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/144,925
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/685,992
 ; FILING DATE: July 25, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: CSHL96-032
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 781-861-6240
 ; TELEFAX: 781-861-9540
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 245 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single

; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-09-144-925-26
 Alignment Scores:
 Pred. No.: 8,64e-173
 Score: 197.00
 Percent Similarity: 97.61%
 Best Local Similarity: 97.61%
 Query Match: 17.31%
 DB: 2
 Gaps: 0
 US-09-719-272-1 (1-3467) x US-09-144-925-26 (1-245)
 QY 1062 ACCGTCCGCTTATCATAGCCGCAAGCTGCTGCAACAGTTCAAGACCGGTGTGAAC 1121
 Db 1 ThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsnArgLeuValAsn 20
 QY 1122 ATCATGCCCTAAGAAATTGACCCGCTGTGTCTGACAGCCCATCCGCTGTGTGAAGGCTCT 1181
 Db 21 IleMetProTyrGlnLeuThrArgValCysLeuGlnProIleArgGlyValGlnGlySer 40
 QY 1182 GACTACATCAATGCCAGCTTCTGTGATGTTATAGACAGACAGAGGCTTACATAGCTACA 1241
 Db 41 AspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnGlnLysAlaTyrIleAlaThr 60
 QY 1242 CAGGGGCTCTGGCAGAGGACACCGAGACTTGTGCGCATGCTATGGAGAGACAAATTC 1301
 Db 61 GlnGlyProLeuAlaGlnSerThrGlnAspPheThrArgMetLeuThrGlnHisAsnSer 80
 QY 1302 ACCATCATGCTCATGCTGACCAAGCTTGGGAGATGGGAGAAATGCCACCGATAC 1361
 Db 81 ThrIleIleValMetLeuThrLysLeuArgGlnMetGlyArgGlnLysCysHisGlnTyr 100
 QY 1362 TGGCCACAGAGAGGCTTGTGCTGCTCAAGTACTTGTGTGACCGGATGCTGAGTAC 1421
 Db 101 TTPProAlaGlnArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyr 120
 QY 1422 AACATGCCCGCACTATATCTCGTGAAGTTCAAGTCCAGATGCCCGGATGGGAGTCA 1481
 Db 121 AsnMetProGlnTyrIleLeu-----PheLysValIleThrAspAlaArgAspGlyGlnSer 138
 QY 1482 AGGACAAATCCGGCAGTCCAGTTCAAGACTGGCCAGAGCAGGGCGTCCCAAGACAGGC 1541
 Db 139 ArgThrIleArgGlnPheGlnPheThrAspIleProGlnGlnGlnValProLysThrGly 158
 QY 1542 GAGGATTCATTGACTTCACTCCGCGAGTGCATTAAGACCAAGACGACTTTGACAGGAT 1601
 Db 159 GluGlyPheIleAspPheIleGlyGlnValHisLysThrLysGlnGlnPheGlyGlnAsp 178
 QY 1602 GGGCCTATACAGGTGACAGTGCAGTGCAGGCGGCGGCGGAGTTCATCACTCTG 1661
 Db 179 GlyProIleThrValHisCysSerAlaGlyValGlyAspThrGlyValPheIleThrLeu 198
 QY 1662 AGCATGCTCCTGAGCGCATGCGCTATGAAGGCGTGTGACATGTTTCAAGCCGTGAAG 1721
 Db 199 SerIleValLeuGlnArgMetArgTyrGlnGlyValValAspMetPheGlnThrValLys 218
 QY 1722 ACCCTGCTTACAGAGGCTCTGCTGCAAGTGTGACAGACAGAGACCAAGTACAGTGTAC 1781
 Db 219 ThrLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGlnTyrGlnLeuGlyTyr 238
 QY 1782 CGTGGGCGCTGGAGTACCTC 1802
 Db 239 ArgAlaAlaLeuGlnTyrLeu 245
 RESULT 8
 US-08-202-389-21
 ; Sequence 21, Application US/08202389
 ; Patent No. 5536636
 ; GENERAL INFORMATION:
 ; APPLICANT: Freeman Jr., Robert M.
 ; APPLICANT: Plutsky, Jorge

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      Db      81 GlnPheGlyGlnAlaPheGlyProIleThrValHisCysSerAlaGly 95
      RESULT 9
      US-08-447-464-3
      ; Sequence 3, Application US/08447464
      ; Patent No. 5840842
      GENERAL INFORMATION:
      APPLICANT: Schlensing, Joseph
      TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
      NUMBER OF INVENTION: PHOSPHOTRANSFERASE-SIGMA
      NUMBER OF SEQUENCES: 12
      CORRESPONDENCE ADDRESS:
      ADDRESSEE: Pennie & Edmonds
      STREET: 1155 Avenue of the Americas
      CITY: New York
      STATE: New York
      COUNTRY: U.S.A.
      ZIP: 10036-2711
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patent Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/447,464
      FILING DATE: 24-MAY-1995
      CLASSIFICATION: 435
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 08/130,570
      FILING DATE: 01-OCT-1993
      ATTORNEY/AGENT INFORMATION:
      NAME: Mastrock, S. Leslie
      REGISTRATION NUMBER: 18,872
      REFERENCE/DOCKET NUMBER: 7683-043
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 212-790-9090
      TELEFAX: 212-869-8664/5741
      TELEX: 66141 PENNIE
      INFORMATION FOR SEQ ID NO: 3:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 1501 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      US-08-447-464-3
      Alignment Scores:
      Pred. No.: 8.56e-46 Length: 1501
      Score: 59.00 Matches: 59
      Percent Similarity: 100.00% Conservative: 0
      Best Local Similarity: 100.00% Mismatches: 0
      Query Match: 5.18% Indels: 0
      Gaps: 0
      DB:
      US-09-719-272-1 (1-3467) x US-08-447-464-3 (1-1501)
      QY 1311 GTCATGTCGACCAAGCTTCGGAGATGGCGAGGAATGCCAAGTACTGGCCGACA 1370
      Db 1330 VALMCTLEUTHIRIVSLLEARGGLMDELGYARGIUYSCYSHLSGINTYTRPProAla 1349
      QY 1371 GAGGCGCTTGCTCGCTACCAAGTACTTTGTGTGTAACCCGAGTGGCTGAGTACCAATGCC 1430
      Db 1350 GUAAGSERRALAIRTYGLINTYRheValValaAPrometAlaIGINTYRasmNePro 1365
      QY 1431 CAGTATATCCGTCGAGTCAAGGTCAAGATGCCCGAGATGGCGACTCAAGACA 1487
      Db 1370 GINTYRIELEuARGIuPhelyValIthrSPAlaAgaApGlyGlnSerArgThr 1388
      RESULT 10
      US-08-716-679-3
      ; Sequence 3, Application US/08716679
      ; Patent No. 5846800
  
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GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,679
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/130,570
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1501 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-716-679-3

Alignment Scores:
Pred. No.: 8,566-46 Length: 1501
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
Gaps: 0
DB: 2

US-09-719-272-1 (1-3467) x US-08-716-679-3 (1-1501)

QY 1311 GTCATGCTGACCAAGCTTCGGAGATGGGACAGGAGAAATGCCACAGTACTGGCCAGCA 1370
DB 1330 ValMetLeuThrIysLeuArgIuMetGIyArgGIuIyCysHieGIuIyTrpProIa 1349
QY 1371 GAGCGCTGCTGCTGCTACCAAGTACTTGTGTTGACCCGATGGCTGAGTCAACAATGCC 1430
DB 1350 GluArgSerAlaArgIyGlnIyTrpPheValIValAspProMetAlaGIuIyTrsMetPro 1369

QY 1431 CAGTATATCTGCGTGGTCAAGTCAAGATGCCGATGCCGAGATGGGCAATCAAGACA 1487
DB 1370 GlnIyTrIleuArgIuPheIyValIThrAspAlaArgAspGIyGlnIserArgThr 1388

RESULT 11
US-08-348-006B-5
Sequence 5, Application US/08348006B
Patent No. 5658756
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSES: J. MARK HAND
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,006B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 189921A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-4720
TELEFAX: 908-594-3905
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1911 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-348-006B-5

Alignment Scores:
Pred. No.: 8,276-46 Length: 1911
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
Gaps: 0
DB: 1

US-09-719-272-1 (1-3467) x US-08-348-006B-5 (1-1911)

QY 1311 GTCATGCTGACCAAGCTTCGGAGATGGGACAGGAGAAATGCCACAGTACTGGCCAGCA 1370
DB 1740 ValMetLeuThrIysLeuArgIuMetGIyArgGIuIyCysHieGIuIyTrpProIa 1759
QY 1371 GAGCGCTGCTGCTGCTACCAAGTACTTGTGTTGACCCGATGGCTGAGTCAACAATGCC 1430
DB 1760 GluArgSerAlaArgIyGlnIyTrpPheValIValAspProMetAlaGIuIyTrsMetPro 1779

QY 1431 CAGTATATCTGCGTGGTCAAGTCAAGATGCCGATGCCGAGATGGGCAATCAAGACA 1487
DB 1780 GlnIyTrIleuArgIuPheIyValIThrAspAlaArgAspGIyGlnIserArgThr 1798

RESULT 12
US-08-800-825A-5
Sequence 5, Application US/08800825A
Patent No. 5866397
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSES: J. MARK HAND - MERCK & CO., INC.
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,657
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/800,825
FILING DATE: 14-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18992DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1911 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-158-657-5

Alignment Scores:
Pred. NO.:
Score: 8.27e-46 Length: 1911
Percent Similarity: 59.00 Matches: 59
Best Local Similarity: 100.00% Conservatave: 0
Query Match: 100.00% Mismatches: 0
DB: 3 Gaps: 0

US-09-719-272-1 (1-3467) x US-09-158-657-5 (1-1911)
QY 1311 GTCATGCTGACCAAGCTTCGAGAGATGGCGAGAGAGAAATGCCACGATGCGCCAGCA 1370
Db |||||
Db 1740 ValMetLeuThrIryIseuAArgIuMeGlyArgGluIyeCysHsIglntYrTpPrcAla 1759
QY 1371 GAGGCGCTGCTGCTGCTACCAAGTACTTTGTTGTGATGCCCATGGCTAGTACCAACATGCC 1430
Db |||||
Db 1760 GlArGserAlaArgIryGlnIryPheValValAspProweIaIagIuIryAsMeIPro 1779
QY 1431 CAGATATCTCTGGGTGATGATTCAGAGTCCAGATCCCGGATGGGCGAGTCAAGGACA 1487
Db |||||
Db 1780 GlnIryIleuAArgIuPheIyValThrAspAlaArgAspGlyGlnserAArgThr 1798

RESULT 14
PCT-US94-10166-5
Sequence 5, Application PC/TUS9410166
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN W. MALLEN III
STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10166
FILING DATE: 09-SEPT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032

```

FILED DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: WALLEN, JOHN W III
REGISTRATION NUMBER: 35403
REFERENCE/DOCKET NUMBER: 16992
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
TELEFAX: 908-594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1911 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-10166-5

Alignment Scores:
Pred. No.: 8,27e-46 Length: 1911
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
Gaps: 0
DB:

US-09-719-272-1 (1-3467) x PCT-US94-10166-5 (1-1911)

QY 1311 GTCATGCTGACCACTTCGGAGATGGGAGAGAAATCCACAGTACTGCGCAGCA 1370
DB 1740 ValMetLeuThrIleuLeuArgGluMetGlyArgGlySerGlySerGlyTrpProAla 1759
QY 1371 GAGCGCTGTGCTGCTACCACTTCTTGTGTGAACCGATGCTGATCAACATGCC 1430
DB 1760 GluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGlnTyrAsnMetPro 1779
QY 1431 CAGTATCCCTGCGGAGTTCAGGTCAAGTGCCTGGGATGGGAGTCAAGGACA 1487
DB 1780 GlnTyrIleuLeuArgGlnPheValThrAspAlaArgAspGlyGlnSerArgThr 1798

RESULT 15
US-08-202-389-22
Sequence 22, Application US/08202389
Patent No. 5536636
GENERAL INFORMATION:
APPLICANT: Freeman Jr., Robert M.
APPLICANT: Plutsky, Jorge
APPLICANT: Neel, Benjamin G.
APPLICANT: Rosenberg, Robert D.
TITLE OF INVENTION: IDENTIFICATION OF NOVEL TYROSINE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Mallitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,389
FILING DATE: 28-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,926
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/829,141

FILED DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/721,112
FILING DATE: 26-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: B192-05WA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-202-389-22

Alignment Scores:
Pred. No.: 1.45e-34 Length: 95
Score: 47.00 Matches: 47
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.13% Indels: 0
Gaps: 0
DB:

US-09-719-272-1 (1-3467) x US-08-202-389-22 (1-95)

QY 1347 AATGGCACCACTACTGCGCAGCAGAGGCGCTGCTGCTACCACTTGTGTGAC 1406
DB 1 LysCysHisGlnTyrTrpProAlaGlnArgSerAlaArgTyrGlnTyrPheValValAsp 20
QY 1407 CCGATGCTGAGTACCAACATGCCCAATATCTGCGTGAAGTTCAGGTCAAGATGCC 1466
DB 21 ProMetAlaGlnTyrAsnMetProGlnTyrIleuArgGlnPheValThrAspAla 40
QY 1467 CCGGATGGGCACTCAAGGACA 1487
DB 41 ArgAspGlyGlnSerArgThr 47

Search completed: March 9, 2004, 09:13:29
Job time: 64 secs